

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 16, 2004, 10:12:21 ; Search time 23 Seconds
(without alignments)
918.044 Million cell updates/sec

Title: US-10-063-523-22
Perfect score: 2109
Sequence: 1 MEGESTSAVLGFLGALAF.....TDEIEKMGGEVSRSTPT 409

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/aa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	778	36.9	151	4	US-09-621-976-3917
2	122	5.8	1087	4	US-09-914-259-12
3	122	5.8	2482	1	US-08-328-284-6
4	122	5.8	3248	1	US-08-353-700-1
5	122	5.8	3248	5	PCT-US95-16216-1
6	111.5	5.3	1038	4	US-08-334-179A-2
7	111.5	5.3	1038	4	US-09-908-500A-2
8	111	5.3	1972	4	US-08-875-435B-4
9	110.5	5.2	1038	3	US-09-541-782-4
10	110.5	5.2	1038	4	US-09-723-820-4
11	110.5	5.2	1038	4	US-10-270-085-4
12	110	5.2	530	4	US-08-979-608A-8
13	110	5.2	530	4	US-09-517-849-8
14	110	5.2	530	4	US-09-616-289-8
15	110	5.2	546	4	US-09-616-289-44
16	109.5	5.2	1038	4	US-08-334-179A-8
17	109	5.2	1972	4	US-08-875-435B-3
18	108.5	5.1	1257	1	US-08-049-783-2
19	108.5	5.1	1257	1	US-08-158-232-6
20	108.5	5.1	1257	1	US-08-304-626-6
21	108.5	5.1	1257	2	US-08-316-301A-6
22	108.5	5.1	1257	1	US-08-611-928-6
23	108.5	5.1	1257	3	US-09-173-891-6
24	108.5	5.1	1257	3	US-09-076-137-6
25	108.5	5.1	1257	4	US-09-738-363-6
26	108.5	5.1	1257	5	PCT-US92-03624-6
27	108.5	5.1	2662	4	US-09-595-684B-31

Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4820, Ap
Sequence 2, Appli
Sequence 11, Appli
Sequence 6618, Ap
Sequence 72, Appli
Sequence 21, Appli
Sequence 16, Appli
Sequence 2, Appli
Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-621-976-3917
; Sequence 3917, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3917
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19..-1
US-09-621-976-3917

Query Match 36.9%; Score 778; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.9e-64;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGESTSAVLGFLGALAFQHLNTSDTEGFLGVEKGNISITDSOMDVEVYITID 60
Db 1 MEGESTSAVLGFLGALAFQHLNTSDTEGFLGVEKGNISITDSOMDVEVYITID 60
QY 61 IQKYPICYOLFYSNYSSEVNEQALKKILSNVKNVGVGKFRHSDQIMTFRERLLHKN 120
Db 61 IQKYPICYOLFYSNYSSEVNEQALKKILSNVKNVGVGKFRHSDQIMTFRERLLHKN 120
QY 121 LQEHFSNQLVFLLLTPSIITSCSTHRLH 151
Db 121 LQEHFSNQLVFLLLTPSIITSCSTHRLH 151

RESULT 2
US-09-914-259-12
; Sequence 12, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hymen, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999

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OM protein - protein search, using sw model

Run on: April 16, 2004, 10:16:01 ; Search time 46 Seconds
(without alignments)
2805.368 Million cell updates/sec

Title: US-10-063-523-22

Perfect score: 409
Sequence: 1 MEGSSTAVLGSFVLGALAF.....TDEIEKMGFGYRSPTF 409

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 6

Total number of hits satisfying chosen parameters: 5503

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organella.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertibrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	263	64.3	300	4 QH811	QH811 homo sapien
2	238	58.2	300	4 QH9N4	QH9N4 homo sapien
3	19	4.6	212	11 Q8BT9	Q8BT9 mus musculus
4	19	4.6	261	11 Q8BF6	Q8BF6 mus musculus
5	19	4.6	407	11 Q8BP28	Q8BP28 mus musculus
6	16	3.9	298	11 Q8K2T7	Q8K2T7 mus musculus
7	9	2.2	546	17 Q28405	Q28405 archaeoglob
8	8	2.0	128	16 Q83R71	Q83R71 shigella fl
9	8	2.0	132	15 Q8AD48	Q8AD48 human immun
10	8	2.0	246	16 Q8VD88	Q8VD88 bruceella me
11	8	2.0	250	16 Q8FUN2	Q8FUN2 bruceella su
12	8	2.0	297	16 Q9A4B6	Q9A4B6 caulobacter
13	8	2.0	301	4 Q8NCW9	Q8NCW9 homo sapien
14	8	2.0	312	3 Q94401	Q94401 schizosacch
15	8	2.0	322	6 Q28621	Q28621 oryctolagus
16	8	2.0	326	12 Q9IP73	Q9IP73 human rotav

17	8	2.0	359	4 Q9H297	Q9H297 homo sapien
18	8	2.0	360	6 Q9GK69	Q9GK69 oryctolagus
19	8	2.0	402	6 Q28622	Q28622 oryctolagus
20	8	2.0	419	4 Q15018	Q15018 homo sapien
21	8	2.0	442	16 Q8UBL9	Q8UBL9 agrobacteri
22	8	2.0	452	4 Q9Y681	Q9Y681 homo sapien
23	8	2.0	470	10 Q9M306	Q9M306 arabidopsis
24	8	2.0	639	6 Q28623	Q28623 oryctolagus
25	8	2.0	690	4 Q9HCH1	Q9HCH1 homo sapien
26	8	2.0	892	16 Q7V419	Q7V419 prochloroco
27	8	2.0	1309	10 Q9LUG9	Q9LUG9 arabidopsis
28	8	2.0	1309	10 Q8GZA2	Q8GZA2 arabidopsis
29	7	1.7	81	2 P72388	P72388 staphylococ
30	7	1.7	88	15 Q90A88	Q90A88 human immun
31	7	1.7	88	15 Q9DR26	Q9DR26 human immun
32	7	1.7	91	15 Q90BJ1	Q90BJ1 human immun
33	7	1.7	92	16 Q9KF07	Q9KF07 bacillus ha
34	7	1.7	100	10 Q93ZJ3	Q93ZJ3 arabidopsis
35	7	1.7	101	16 Q8NL05	Q8NL05 xanthomonas
36	7	1.7	103	10 Q9LQ1	Q9LQ1 arabidopsis
37	7	1.7	104	16 Q8ZIX9	Q8ZIX9 yersinia pe
38	7	1.7	105	16 Q8XGT8	Q8XGT8 salmonella
39	7	1.7	108	10 Q9LWQ0	Q9LWQ0 oryza sativ
40	7	1.7	110	16 Q8E6E9	Q8E6E9 streptococ
41	7	1.7	114	16 Q8A302	Q8A302 bacteroides
42	7	1.7	115	15 Q7ZEP5	Q7ZEP5 human immun
43	7	1.7	116	12 Q8V6V7	Q8V6V7 halovirus h
44	7	1.7	116	12 Q7TDP0	Q7TDP0 halovirus h
45	7	1.7	136	16 Q8Y4K1	Q8Y4K1 listeria mo
46	7	1.7	136	17 Q9UZRS	Q9UZRS pyrococcus
47	7	1.7	137	17 Q8U1N2	Q8U1N2 pyrococcus
48	7	1.7	138	16 Q93MB9	Q93MB9 clostridium
49	7	1.7	140	5 Q9XX55	Q9XX55 caenorhabdi
50	7	1.7	143	2 Q9S8S4	Q9S8S4 plesiomonas
51	7	1.7	144	16 Q99F14	Q99F14 bradyrhizob
52	7	1.7	145	16 Q8EB62	Q8EB62 shewanella
53	7	1.7	153	16 Q8UIG7	Q8UIG7 agrobacteri
54	7	1.7	153	16 Q8D1E4	Q8D1E4 yersinia pe
55	7	1.7	154	16 Q8G8S7	Q8G8S7 rhizobium l
56	7	1.7	154	16 Q92SJ9	Q92SJ9 rhizobium m
57	7	1.7	154	16 Q8YEUI	Q8YEUI bruceella me
58	7	1.7	154	16 Q8G2Z6	Q8G2Z6 bruceella su
59	7	1.7	155	2 Q9AKF2	Q9AKF2 rickettsia
60	7	1.7	156	10 Q9LIZ1	Q9LIZ1 oryza sativ
61	7	1.7	158	2 Q9RN96	Q9RN96 streptococ
62	7	1.7	173	8 Q94UY8	Q94UY8 pluvialis s
63	7	1.7	173	8 Q958D2	Q958D2 tinamus maj
64	7	1.7	174	8 Q958A6	Q958A6 pterocnemia
65	7	1.7	177	12 Q57255	Q57255 vaccinia vi
66	7	1.7	181	12 Q8QMP4	Q8QMP4 cowpox viru
67	7	1.7	181	12 Q9JFT2	Q9JFT2 ectromelia
68	7	1.7	181	16 Q8R8X5	Q8R8X5 thermoanaer
69	7	1.7	182	12 Q8V4S0	Q8V4S0 monkeypox v
70	7	1.7	182	12 Q8KGA1	Q8KGA1 vaccinia vi
71	7	1.7	182	12 Q72743	Q72743 cowpox viru
72	7	1.7	185	10 Q22194	Q22194 arabidopsis
73	7	1.7	187	10 Q93674	Q93674 medicago sa
74	7	1.7	190	16 Q9K8Q2	Q9K8Q2 bacillus ha
75	7	1.7	201	5 Q8SW02	Q8SW02 encephalito
76	7	1.7	202	5 Q77378	Q77378 plasmodium
77	7	1.7	216	5 Q9N9M4	Q9N9M4 leishmania
78	7	1.7	220	2 Q98436	Q98436 streptococ
79	7	1.7	221	17 Q8UOK7	Q8UOK7 pyrococcus
80	7	1.7	227	16 Q8ED42	Q8ED42 shewanella
81	7	1.7	228	5 Q01329	Q01329 caenorhabdi
82	7	1.7	236	16 Q8Y2U4	Q8Y2U4 raietonia s
83	7	1.7	237	16 Q9K6G9	Q9K6G9 bacillus ha
84	7	1.7	239	5 Q9N7Q3	Q9N7Q3 lymanaea sta
85	7	1.7	242	16 Q816W1	Q816W1 bacillus ce
86	7	1.7	244	11 Q8KIL4	Q8KIL4 mus musculus
87	7	1.7	244	11 Q90I50	Q90I50 mus musculus
88	7	1.7	245	6 Q95LW2	Q95LW2 macaca fasc
89	7	1.7	245	10 Q9SNW9	Q9SNW9 arabidopsis

90	7	1.7	247	5	Q8IB21	Q8IB21 plasmodium	163	7	1.7	393	10	O64911	O64911 solanum tub
91	7	1.7	247	16	Q82VV9	Q82vv9 nitrosomona	164	7	1.7	395	16	Q8RA61	Q8ra61 thermocanaer
92	7	1.7	254	16	Q97J11	Q97j11 clostridium	165	7	1.7	397	16	Q8ISN9	Q8isn9 bacillus an
93	7	1.7	257	16	Q97Q44	Q97q44 streptococc	166	7	1.7	398	2	O87I05	O87i05 streptococc
94	7	1.7	258	2	Q9ALL2	Q9all2 escherichia	167	7	1.7	398	2	O87I08	O87i08 streptococc
95	7	1.7	264	2	Q7WZ08	Q7wz08 lysobacter	168	7	1.7	398	2	Q9R7M5	Q9r7m5 streptococc
96	7	1.7	266	16	Q97QX9	Q97qx9 streptococc	169	7	1.7	398	2	O87I03	O87i03 streptococc
97	7	1.7	266	16	Q8ZJC0	Q8zjc0 yersinia pe	170	7	1.7	398	2	Q9S7M8	Q9s7m8 streptococc
98	7	1.7	269	10	Q9LH18	Q9lh18 arabidopsis	171	7	1.7	398	2	Q9R7M7	Q9r7m7 streptococc
99	7	1.7	270	16	Q8D8F1	Q8d8f1 vibrio vuln	172	7	1.7	400	4	Q7Z495	Q7z495 homo sapien
100	7	1.7	278	16	Q8PD22	Q8pe22 xanthomonas	173	7	1.7	401	5	Q8I0S6	Q8i0s6 drosophila
101	7	1.7	278	16	Q8CWG3	Q8cwg3 yersinia pe	174	7	1.7	401	10	Q84Y17	Q84y17 solanum tub
102	7	1.7	279	16	Q8POZ0	Q8pzo0 xanthomonas	175	7	1.7	401	16	Q7V969	Q7v969 prochloroc
103	7	1.7	281	16	Q8ZEL8	Q8zel8 lotus japon	176	7	1.7	404	16	O84Z59	O84z59 chlamydia t
104	7	1.7	282	10	Q9ZEL8	Q9zel8 lotus japon	177	7	1.7	404	16	O8XZ64	O8xz64 ralstonia s
105	7	1.7	283	8	Q9B8U7	Q9b8u7 schistosoma	178	7	1.7	406	16	O894W1	O894w1 clostridium
106	7	1.7	283	8	Q9B8U4	Q9b8u4 schistosoma	179	7	1.7	410	2	O83X68	O83x68 streptomyc
107	7	1.7	285	11	Q8BIB1	Q8bib1 mus musculu	180	7	1.7	410	16	Q8ZIS2	Q8zis2 yersinia pe
108	7	1.7	285	10	Q8EAG1	Q8eag1 dictyosteli	181	7	1.7	410	16	Q9VPG5	Q9vpg5 drosophila
109	7	1.7	285	10	O82587	O82587 arabidopsis	182	7	1.7	417	5	Q9VPG5	Q9vpg5 drosophila
110	7	1.7	291	2	Q8R8C1	Q8r8c1 borrelia bu	183	7	1.7	418	16	Q8RFW2	Q8rfw2 fusobacteri
111	7	1.7	291	2	Q8R8C1	Q8r8c1 borrelia bu	184	7	1.7	418	16	Q9VPG4	Q9vpg4 drosophila
112	7	1.7	294	10	Q8S330	Q8s330 acetabulari	185	7	1.7	419	5	Q9W3C3	Q9w3c3 drosophila
113	7	1.7	294	16	Q8S330	Q8s330 acetabulari	186	7	1.7	425	5	Q9W3C3	Q9w3c3 drosophila
114	7	1.7	298	8	Q9B8G3	Q9b8g3 heterodoxus	187	7	1.7	425	16	O82TU8	O82tu8 nitrosomona
115	7	1.7	304	17	Q9HNT9	Q9hnt9 halobacteri	188	7	1.7	425	16	O82TU8	O82tu8 nitrosomona
116	7	1.7	310	2	O52743	O52743 streptococc	189	7	1.7	427	16	O82TU8	O82tu8 nitrosomona
117	7	1.7	310	2	O52743	O52743 streptococc	190	7	1.7	427	16	O82TU8	O82tu8 nitrosomona
118	7	1.7	310	2	O52743	O52743 streptococc	191	7	1.7	427	16	O82TU8	O82tu8 nitrosomona
119	7	1.7	310	2	O52738	O52738 streptococc	192	7	1.7	431	16	O82TU8	O82tu8 nitrosomona
120	7	1.7	310	2	O52738	O52738 streptococc	193	7	1.7	431	16	O82TU8	O82tu8 nitrosomona
121	7	1.7	314	9	Q7Y547	Q7y547 bacterioph	194	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
122	7	1.7	314	9	Q7Y547	Q7y547 bacterioph	195	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
123	7	1.7	316	5	Q9VWL5	Q9vwl5 drosophila	196	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
124	7	1.7	319	4	O80477	O80477 homo sapien	197	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
125	7	1.7	321	11	O70267	O70267 rattus norv	198	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
126	7	1.7	322	17	Q70UG4	Q70ug4 sulfolobus	199	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
127	7	1.7	324	16	Q8E515	Q8e515 streptococc	200	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
128	7	1.7	324	16	Q8DZT8	Q8dz8 streptococc	201	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
129	7	1.7	324	16	Q7WQH6	Q7wqh6 bordetella	202	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
130	7	1.7	324	16	Q7WQH1	Q7wqh1 bordetella	203	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
131	7	1.7	327	8	Q9C8S8	Q9c8s8 naegleria g	204	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
132	7	1.7	329	3	Q8JLIC9	Q8jlic9 oncorhynch	205	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
133	7	1.7	331	13	Q8GZV9	Q8gzv9 oryza sativ	206	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
134	7	1.7	332	10	Q9NR44	Q9nr44 homo sapien	207	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
135	7	1.7	334	4	Q9BUL1	Q9bul1 homo sapien	208	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
136	7	1.7	334	13	Q801T9	Q801t9 brachydanio	209	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
137	7	1.7	346	16	Q89L60	Q89l60 bradyrhizob	210	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
138	7	1.7	346	16	Q89L60	Q89l60 bradyrhizob	211	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
139	7	1.7	350	5	Q8SVL1	Q8svl1 encephalito	212	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
140	7	1.7	351	9	O80202	O80202 methanobact	213	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
141	7	1.7	351	16	Q81B65	Q81b65 bacillus ce	214	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
142	7	1.7	357	4	O15338	O15338 homo sapien	215	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
143	7	1.7	357	16	Q88H70	Q88h70 pseudomonas	216	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
144	7	1.7	359	4	P78410	P78410 homo sapien	217	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
145	7	1.7	359	10	Q81IJ0	Q81ij0 oryza sativ	218	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
146	7	1.7	359	10	Q9EQ03	Q9eq03 mus musculu	219	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
147	7	1.7	361	5	O41157	O41157 caenorhabdi	220	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
148	7	1.7	361	12	Q84574	Q84574 paramesum	221	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
149	7	1.7	362	17	Q8TN83	Q8tn83 methanosarc	222	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
150	7	1.7	362	17	Q8RT95	Q8rt95 streptococc	223	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
151	7	1.7	367	17	Q978X8	Q978x8 thermoplas	224	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
152	7	1.7	371	16	Q985Z4	Q985z4 rhizobium l	225	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
153	7	1.7	371	16	Q985Z4	Q985z4 rhizobium l	226	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
154	7	1.7	378	2	Q8KUG7	Q8kug7 actinomyne	227	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
155	7	1.7	380	5	Q9VPF7	Q9vpf7 drosophila	228	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
156	7	1.7	385	10	O80521	O80521 arabidopsis	229	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
157	7	1.7	386	16	O50729	O50729 borrelia bu	230	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
158	7	1.7	387	16	O82B97	O82b97 streptomyc	231	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
159	7	1.7	391	16	O81KT4	O81kt4 bacillus an	232	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
160	7	1.7	391	16	O81FJ9	O81fj9 bacillus ce	233	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
161	7	1.7	391	16	O817A5	O817a5 bacillus ce	234	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
162	7	1.7	392	16	O82XZ1	O82xz1 nitrosomona	235	7	1.7	432	16	O82TU8	O82tu8 nitrosomona
163	7	1.7	393	10	O64911	O64911 solanum tub	163	7	1.7	393	10	O64911	O64911 solanum tub
164	7	1.7	395	16	Q8RA61	Q8ra61 thermocanaer	164	7	1.7	395	16	Q8RA61	Q8ra61 thermocanaer
165	7	1.7	397	16	Q8ISN9	Q8isn9 bacillus an	165	7	1.7	397	16	Q8ISN9	Q8isn9 bacillus an
166	7	1.7	398	2	O87I05	O87i05 streptococc	166	7	1.7	398	2	O87I05	O87i05 streptococc
167	7	1.7	398	2	O87I08	O87i08 streptococc	167	7	1.7	398	2	O87I08	O87i08 streptococc
168	7	1.7	398	2	Q9R7M5	Q9r7m5 streptococc	168	7	1.7	398	2	Q9R7M5	Q9r7m5 streptococc
169	7	1.7	398	2	O87I03	O87i03 streptococc	169	7	1.7	398	2	O87I03	O87i03 streptococc
170	7	1.7	398	2	Q9S7M8	Q9s7m8 streptococc	170	7	1.7	398	2	Q9S7M8	Q9s7m8 streptococc
171	7	1.7	398	2	Q9R7M7	Q9r7m7 streptococc	171	7	1.7	398	2	Q9R7M7	Q9r7m7 streptococc
172	7	1.7	400	4	Q7Z495	Q7z495 homo sapien	172	7	1.7	400	4	Q7Z495	Q7z495 homo sapien
173	7	1.7	401	5	Q8I0S6	Q8i0s6 drosophila	173	7	1.7	401	5	Q8I0S6	Q8i0s6 drosophila
174	7	1.7	401	10	Q84Y17	Q84y17 solanum tub	174	7	1.7	401	10	Q84Y17	Q84y17 solanum tub
175	7	1.7	401	16	Q7V969	Q7v969 prochloroc	175	7	1.7	401	16	Q7V969	Q7v969 prochloroc
176	7	1.7	404	16	O84Z59	O84z59 chlamydia t	176	7	1.7	404	16	O84Z59	O84z59 chlamydia t
177	7	1.7	404	16	O8XZ64	O8xz64 ralstonia s	177	7	1.7	404	16	O8XZ64	O8xz64 ralstonia s
178	7	1.7	406	16	O894W1	O894w1 clostridium	178	7	1.7	406	16	O894W1	O894w1 clostridium
179	7	1.7	410	2	O83X68	O83x68 streptomyc	179	7	1.7	410	2	O83X68	O83x68 streptomyc
180	7	1.7	410	16	Q8ZIS2	Q8zis2 yersinia pe	180	7	1.7	410	16	Q8ZIS2	Q8zis2 yersinia pe
181	7	1.7	410	16	Q9VPG5	Q9vpg5 drosophila	181	7	1.7	410	16	Q9VPG5	Q9vpg5 drosophila
182	7	1.7	417	5	Q9VPG5	Q9vpg5 drosophila	182	7	1.7	417	5	Q9VPG5	Q9vpg5 drosophila
183	7	1.7	418	16	Q8RFW2	Q8rfw2 fusobacteri	183	7	1.7	418	16	Q8RFW2	Q8rfw2 fusobacteri
184	7	1.7	419	5	Q9VPG4	Q9vpg4 drosophila	184	7	1.7	419	5	Q9VPG4	Q9vpg4 drosophila
185	7	1.7	425	5	Q9W3C3	Q9w3c3 drosophila	185	7	1.7	425	5	Q9W3C3	Q9w3c3 drosophila
186	7	1.7	425	16	O82TU8	O82tu8 nitrosomona	186	7	1.7	425	16	O82TU8	O82tu8 nitrosomona

236	7	1.7	572	16	Q87C92	Q87C92 xylella fas	309	7	1.7	1375	4	Q8IX65	Q8IX65 homo sapien
237	7	1.7	573	5	Q97211	Q97211 leishmania	310	7	1.7	1378	4	Q8WXR4	Q8WXR4 homo sapien
238	7	1.7	583	16	Q8VNS5	Q8VNS5 anabaena sp	311	7	1.7	1288	4	Q8IZA8	Q8IZA8 homo sapien
239	7	1.7	588	2	Q8GPLL	Q8GPLL streptococc	312	7	1.7	1314	4	Q8IX66	Q8IX66 homo sapien
240	7	1.7	588	2	Q8GPK6	Q8GPK6 streptococc	313	7	1.7	1330	10	Q8LI60	Q8LI60 oryza sativ
241	7	1.7	589	16	Q8UIZ5	Q8UIZ5 agrobacteri	314	7	1.7	1341	4	Q8IX67	Q8IX67 homo sapien
242	7	1.7	591	11	Q8UOW4	Q8UOW4 mus musculu	315	7	1.7	1346	10	Q8GU60	Q8GU60 oryza sativ
243	7	1.7	593	5	Q8TSL2	Q8TSL2 anopheles g	316	7	1.7	1353	4	Q9Y4B5	Q9Y4B5 homo sapien
244	7	1.7	608	2	Q84951	Q84951 streptococc	317	7	1.7	1357	10	Q8GU61	Q8GU61 oryza sativ
245	7	1.7	617	16	Q32206	Q32206 bacillus su	318	7	1.7	1388	13	Q91785	Q91785 xenopus lae
246	7	1.7	618	16	Q8P6Q2	Q8P6Q2 xanthomonas	319	7	1.7	1426	10	Q8L4X0	Q8L4X0 oryza sativ
247	7	1.7	635	2	Q19G7	Q19G7 streptomyc	320	7	1.7	1431	11	Q91ZD9	Q91ZD9 ratu
248	7	1.7	642	16	Q8A2G4	Q8A2G4 bacteroides	321	7	1.7	1496	4	Q9H226	Q9H226 homo sapien
249	7	1.7	651	17	Q9YCF0	Q9YCF0 aeropyrum p	322	7	1.7	1496	11	Q91ZD8	Q91ZD8 ratu
250	7	1.7	661	16	Q88B88	Q88B88 pseudomonas	323	7	1.7	1568	4	Q6O486	Q6O486 homo sapien
251	7	1.7	674	16	Q9HT30	Q9HT30 pseudomonas	324	7	1.7	1574	11	Q9QZC2	Q9QZC2 mus musculu
252	7	1.7	675	16	Q7U958	Q7U958 synechococc	325	7	1.7	1667	5	Q18901	Q18901 caenorhabdi
253	7	1.7	689	17	Q26380	Q26380 methanobact	326	7	1.7	1669	11	Q9QZS0	Q9QZS0 mus musculu
254	7	1.7	693	17	Q779A5	Q779A5 thermoplasm	327	7	1.7	1670	12	Q3IR67	Q3IR67 cucumbe
255	7	1.7	714	16	Q87HC1	Q87HC1 vibrio para	328	7	1.7	1670	12	Q91LR4	Q91LR4 zucchini
256	7	1.7	718	5	Q9NEM5	Q9NEM5 caenorhabdi	329	7	1.7	1670	12	Q91LR4	Q91LR4 zucchini
257	7	1.7	719	2	Q9RET3	Q9RET3 streptococc	330	7	1.7	1672	16	Q8Y366	Q8Y366 rai
258	7	1.7	727	2	Q57114	Q57114 streptococc	331	7	1.7	1672	16	Q8Y366	Q8Y366 rai
259	7	1.7	727	5	Q17436	Q17436 caenorhabdi	332	7	1.7	1919	10	Q8LRK9	Q8LRK9 arabidopsi
260	7	1.7	728	17	Q59093	Q59093 pyrococcus	333	7	1.7	1994	10	Q9LP19	Q9LP19 arabidopsi
261	7	1.7	731	4	Q8409	Q8409 homo sapien	334	7	1.7	2838	16	Q891C5	Q891C5 clostridium
262	7	1.7	743	16	Q87Y23	Q87Y23 pseudomonas	335	7	1.7	3013	5	Q81JZ5	Q81JZ5 plasmodium
263	7	1.7	745	11	Q7TS74	Q7TS74 mus musculu	336	7	1.7	3507	16	Q7UNR7	Q7UNR7 rhodopirell
264	7	1.7	749	11	Q8BXW0	Q8BXW0 mus musculu	337	7	1.7	3770	16	Q87G75	Q87G75 vibrio para
265	7	1.7	754	16	Q89V88	Q89V88 bradyrhizob	338	7	1.7	4293	11	Q8H852	Q8H852 mus musculu
266	7	1.7	764	10	Q49371	Q49371 arabidopsi	339	7	1.7	8081	5	Q7Z120	Q7Z120 caenorhabdi
267	7	1.7	767	13	Q91215	Q91215 oncorhynch	340	7	1.7	9196	5	Q81Q87	Q81Q87 drosophila
268	7	1.7	775	5	Q9Y015	Q9Y015 plasmodium	341	6	1.7	10061	4	Q81JZ1	Q81JZ1 plasmodium
269	7	1.7	781	2	Q52753	Q52753 ruminococcu	342	6	1.5	19	4	Q8WTX6	Q8WTX6 homo sapien
270	7	1.7	783	10	Q8H1B5	Q8H1B5 arabidopsi	343	6	1.5	29	16	Q8ZQW0	Q8ZQW0 salmonella
271	7	1.7	783	10	Q9C5L5	Q9C5L5 arabidopsi	344	6	1.5	29	16	Q8X2E5	Q8X2E5 escherichia
272	7	1.7	783	17	Q8TT9	Q8TT9 methanosa	345	6	1.5	35	16	Q7UGL8	Q7UGL8 rhodopirell
273	7	1.7	784	16	Q9TR57	Q9TR57 streptococc	346	6	1.5	36	16	Q87GE2	Q87GE2 vibrio para
274	7	1.7	784	16	Q8DQ30	Q8DQ30 streptococc	347	6	1.5	39	16	Q7UQD8	Q7UQD8 rhodopirell
275	7	1.7	785	10	Q23072	Q23072 arabidopsi	348	6	1.5	45	10	P82191	P82191 spinacia ol
276	7	1.7	794	5	Q8NMJ4	Q8NMJ4 strongyloce	349	6	1.5	45	16	Q8F630	Q8F630 leptospira
277	7	1.7	796	16	Q8A5U3	Q8A5U3 bacteroides	350	6	1.5	45	16	Q8F630	Q8F630 leptospira
278	7	1.7	810	12	Q8JS13	Q8JS13 phthorimaea	351	6	1.5	46	4	Q9NF41	Q9NF41 homo sapien
279	7	1.7	811	10	Q9SPX2	Q9SPX2 arabidopsi	352	6	1.5	46	16	Q8EIS6	Q8EIS6 streptomyc
280	7	1.7	811	5	Q8JLL1	Q8JLL1 caenorhabdi	353	6	1.5	47	16	Q9RJN2	Q9RJN2 enterococc
281	7	1.7	827	11	Q8CFM7	Q8CFM7 mesocricetu	354	6	1.5	47	16	Q8Z2V1	Q8Z2V1 enterococc
282	7	1.7	860	12	Q3RW26	Q3RW26 melanoplus	355	6	1.5	49	2	Q9EVO6	Q9EVO6 escherichia
283	7	1.7	864	10	Q9ZT97	Q9ZT97 arabidopsi	356	6	1.5	52	12	Q7T702	Q7T702 equine rota
284	7	1.7	869	5	Q94174	Q94174 caenorhabdi	357	6	1.5	52	12	Q7T6Z7	Q7T6Z7 equine rota
285	7	1.7	873	10	Q84YV7	Q84YV7 oryza sativ	358	6	1.5	53	8	Q34180	Q34180 cepaea nemo
286	7	1.7	878	4	Q86TB1	Q86TB1 homo sapien	359	6	1.5	55	5	Q7YVY2	Q7YVY2 trypanosoma
287	7	1.7	897	5	Q9V329	Q9V329 caenorhabdi	360	6	1.5	55	10	Q86688	Q86688 zea mays (m
288	7	1.7	897	5	Q9V329	Q9V329 caenorhabdi	361	6	1.5	58	16	Q7UF91	Q7UF91 rhodopirell
289	7	1.7	903	5	Q8LDV9	Q8LDV9 plasmodium	362	6	1.5	59	2	Q46573	Q46573 borrelia af
290	7	1.7	913	16	Q822C0	Q822C0 chlamydophi	363	6	1.5	59	2	Q57397	Q57397 borrelia af
291	7	1.7	914	11	Q8CFM8	Q8CFM8 mesocricetu	364	6	1.5	60	4	Q86W00	Q86W00 homo sapien
292	7	1.7	944	17	Q8TPC2	Q8TPC2 methanosa	365	6	1.5	60	10	Q9LFB7	Q9LFB7 arabidopsi
293	7	1.7	950	5	Q9Y100	Q9Y100 drosophila	366	6	1.5	60	16	Q8F7Z5	Q8F7Z5 leptospira
294	7	1.7	972	2	Q43348	Q43348 enterococc	367	6	1.5	61	16	Q89UG3	Q89UG3 staphylococ
295	7	1.7	1053	10	Q4E82	Q4E82 oryza sativ	368	6	1.5	62	10	Q8XFY0	Q8XFY0 chlorella p
296	7	1.7	1065	16	Q820K6	Q820K6 nitrosomona	369	6	1.5	62	16	Q81JY5	Q81JY5 bacillus an
297	7	1.7	1080	5	Q81BB2	Q81BB2 plasmodium	370	6	1.5	62	16	Q817Y6	Q817Y6 bacillus ce
298	7	1.7	1087	5	Q96923	Q96923 dictyosteli	371	6	1.5	63	14	Q95IT4	Q95IT4 uncultured
299	7	1.7	1099	16	Q8FTW9	Q8FTW9 corynebacte	372	6	1.5	63	16	Q88AJ8	Q88AJ8 pseudomonas
300	7	1.7	1113	4	Q96N94	Q96N94 homo sapien	373	6	1.5	64	2	Q9EV37	Q9EV37 legionella
301	7	1.7	1121	12	Q84405	Q84405 peanut bud	374	6	1.5	64	17	Q97XF7	Q97XF7 sulfolobus
302	7	1.7	1166	12	Q9CNC4	Q9CNC4 cucumber gr	375	6	1.5	67	2	Q9F2D2	Q9F2D2 salmonella
303	7	1.7	1166	12	Q91E48	Q91E48 kyuri green	376	6	1.5	67	5	Q7YUP9	Q7YUP9 trypanosoma
304	7	1.7	1166	12	Q911R3	Q911R3 zucchini gr	377	6	1.5	67	10	Q8LRY4	Q8LRY4 oryza sativ
305	7	1.7	1192	4	Q8IX64	Q8IX64 homo sapien	378	6	1.5	67	12	Q9SES1	Q9SES1 kaposi's sa
306	7	1.7	1205	11	Q8CGW1	Q8CGW1 mus musculu	379	6	1.5	67	16	Q8FJV2	Q8FJV2 escherichia
307	7	1.7	1251	4	Q8IX68	Q8IX68 homo sapien	380	6	1.5	69	16	Q8KFA2	Q8KFA2 chlorobium
308	7	1.7	1251	4	Q8IX68	Q8IX68 homo sapien	381	6	1.5	69	16	Q8KFA1	Q8KFA1 chlorobium

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382 1.5 69 16 Q8KF99 Q8kf99 chlorobium
383 1.5 72 16 Q8MR4 Q8mr4 rhizobium l
384 1.5 72 16 Q8JN6 Q8jn6 rhizobium l
385 1.5 74 16 Q8RG7 Q8rg7 thermoanaer
386 1.5 75 4 Q8ETT7 Q8ett7 homo sapien
387 1.5 75 10 Q7XYC7 Q7xc7 triticum ae
388 1.5 75 12 Q8VRF3 Q8vrf3 white spot
389 1.5 76 4 Q8UW4 Q8uw4 homo sapien
390 1.5 76 4 Q8ETH9 Q8eth9 homo sapien
391 1.5 77 16 Q8XU7 Q8ux7 raietonia s
392 1.5 78 2 Q8RMZ3 Q8rmz3 helicobacte
393 1.5 79 16 Q9ASE1 Q9ase1 cryza sativ
394 1.5 79 16 Q8NV1 Q8nv1 bradyrhizob
395 1.5 79 16 Q82RS4 Q82rs4 streptomyce
396 1.5 80 8 Q47957 Q47957 phoxinus eo
397 1.5 80 12 Q93305 Q93305 porcine rep
398 1.5 81 4 Q6P80 Q6p80 homo sapien
399 1.5 81 11 Q99LK5 Q99lk5 mus musculu
400 1.5 82 2 Q9APU8 Q9apu8 pseudomonas
401 1.5 82 17 Q97513 Q97513 sulfolobus
402 1.5 84 11 Q8K517 Q8k517 mus musculu
403 1.5 84 16 Q8JVG8 Q8jvg8 neisseria m
404 1.5 85 2 Q9461 Q9461 mycoplasma
405 1.5 86 12 Q990R4 Q990r4 hepatitis c
406 1.5 89 2 Q45014 Q45014 borrelia bu
407 1.5 89 12 Q55735 Q55735 chilo iride
408 1.5 89 13 Q800D0 Q800d0 salvelinus
409 1.5 90 10 Q9F82 Q9feb2 cryza sativ
410 1.5 90 12 Q8QL19 Q8qli9 sulfolobus
411 1.5 90 16 Q9PB24 Q9pb24 xylella fas
412 1.5 91 16 Q87BU4 Q87bu4 xanthomonas
413 1.5 91 16 Q8PN38 Q8pn38 xanthomonas
414 1.5 91 16 Q8XF33 Q8xf33 salmonella
415 1.5 92 10 Q8M306 Q8m306 silene coni
416 1.5 92 10 Q42488 Q42488 pharbitis n
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422 1.5 95 15 Q9VS15 Q9vs15 human immun
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424 1.5 96 11 Q222B4 Q222b4 mus musculu
425 1.5 97 10 Q8LK32 Q8lk32 chinopyrum
426 1.5 97 12 Q990R3 Q990r3 hepatitis c
427 1.5 97 12 Q990R5 Q990r5 hepatitis c
428 1.5 97 12 Q990R2 Q990r2 hepatitis c
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435 1.5 99 6 Q9XSA8 Q9xsa8 sus scrofa
436 1.5 101 4 Q86YV5 Q86yv5 homo sapien
437 1.5 101 5 Q9N8G1 Q9n8g1 trypanosoma
438 1.5 101 5 Q7YIN0 Q7yir0 cryptospori
439 1.5 102 1 Q07119 Q07119 halobacteri
440 1.5 102 10 Q9LHZ5 Q9lhz5 cryza sativ
441 1.5 102 10 Q8GYP9 Q8gyp9 arabidopsis
442 1.5 102 11 P97517 P97517 phodopus su
443 1.5 102 11 Q9DA17 Q9da17 mus musculu
444 1.5 103 10 Q9XH09 Q9xh09 prunus dulc
445 1.5 103 16 Q9CB6 Q9cb6 bradyrhizob
446 1.5 104 4 Q9UHQ7 Q9uhq7 homo sapien
447 1.5 104 9 Q9BOE5 Q9boe5 staphylococ
448 1.5 104 9 Q8SDQ2 Q8sdq2 staphylococ
449 1.5 104 10 Q04293 Q04293 arabidopsis
450 1.5 104 11 Q9DD24 Q9dd24 mus musculu
451 1.5 104 11 Q9CTI5 Q9cti5 mus musculu
452 1.5 104 16 P73794 P73794 synechocyst
453 1.5 104 16 Q9CLF6 Q9clf6 pasteurella
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455 1.5 104 16 Q8NWJ5 Q8nwj5 staphylococ
456 1.5 104 17 Q9EXB6 Q9exr6 sulfolobus
457 1.5 105 5 Q9U514 Q9u514 manduca sex
458 1.5 105 17 Q27553 Q27553 methanobact
459 1.5 106 2 Q8ELW9 Q8rlw9 chlorobium
460 1.5 106 5 Q917Q5 Q917q5 drosophila
461 1.5 107 10 Q8GS79 Q8gs79 cryza sativ
462 1.5 107 16 Q9PLR9 Q9plr9 chlamydia m
463 1.5 108 2 Q33851 Q33851 thermus the
464 1.5 108 10 Q8RVD9 Q8rvd9 cryza sativ
465 1.5 108 10 Q94HX3 Q94hx3 cryza sativ
466 1.5 108 11 Q7XCR4 Q7xcr4 cryza sativ
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468 1.5 109 16 Q89Y15 Q89y15 bacteroides
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470 1.5 110 16 Q92V18 Q92v18 rhizobium m
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476 1.5 112 2 Q93FL7 Q93fl7 citrobacter
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479 1.5 112 12 Q31B18 Q31b18 budgerigar
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484 1.5 113 5 Q09960 Q09960 caenorhabdi
485 1.5 113 16 Q92M25 Q92m25 rhizobium m
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488 1.5 114 5 Q818F9 Q818f9 trypanosoma
489 1.5 114 5 Q818F8 Q818f8 trypanosoma
490 1.5 114 8 Q97541 Q97541 carduelis c
491 1.5 114 8 Q99238 Q99238 carduelis c
492 1.5 114 16 Q8NRH6 Q8nrh6 corynebacte
493 1.5 115 4 Q81ZE2 Q81ze2 homo sapien
494 1.5 115 10 Q9AWM2 Q9awm2 cryza sativ
495 1.5 115 11 Q9DAS0 Q9das0 mus musculu
496 1.5 116 2 Q7WY10 Q7wy10 streptococ
497 1.5 116 2 Q9X929 Q9x929 bacillus ep
498 1.5 116 4 Q9H1A8 Q9h1a8 homo sapien
499 1.5 116 11 Q8BN17 Q8bn17 mus musculu
500 1.5 116 16 Q7TUC9 Q7tuc9 prochloroco
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ALIGNMENTS

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RESULT 1
Q9H811 PRELIMINARY; PRT; 300 AA.
ID Q9H811
AC Q9H811;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ13614.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Negai K., Sato H., Sugano S., Ishibashi T., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Negahari K.,
RA Masuho Y., Kanehori K.;
RT "NEDO human cDNA sequencing project.";
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RL
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[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Testis;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK023676; BAB14635.1; -.
DR EMBL; BC039573; AAH39573.1; -.
KW Hypothetical protein.
SQ SEQUENCE 300 AA; 34447 MW; A22EF29B4B0FCAFF CRC64;

Query Match 64.3%; Score 263; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 3.1e-267;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 MTFERLLHKNLQEHFNSQDLVFLLLTPSIITSCSTRHLSHYKPKQGLFHRVPLVVA 169
Db 1 MTFERLLHKNLQEHFNSQDLVFLLLTPSIITSCSTRHLSHYKPKQGLFHRVPLVVA 60

QY 170 NLGMSQQLGYKTVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASYLQELKSI 229
Db 61 NLGMSQQLGYKTVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASYLQELKSI 120

QY 230 CKKVEDSQAVDKLVKQVNRKREIEKRGAGIOAAREKNIOKPOENIFLCOALRTFFP 289
Db 121 CKKVEDSQAVDKLVKQVNRKREIEKRGAGIOAAREKNIOKPOENIFLCOALRTFFP 180

QY 290 NSEFLHSCVMSLKNRHSKSSCNYNHLDVVDNLTLMVEHTDIPEASPASTPQIIKHK 347
Db 181 NSEFLHSCVMSLKNRHSKSSCNYNHLDVVDNLTLMVEHTDIPEASPASTPQIIKHK 238

Query Match 58.2%; Score 238; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.7e-241;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 MTFERLLHKNLQEHFNSQDLVFLLLTPSIITSCSTRHLSHYKPKQGLFHRVPLVVA 169
Db 1 MTFERLLHKNLQEHFNSQDLVFLLLTPSIITSCSTRHLSHYKPKQGLFHRVPLVVA 60

QY 170 NLGMSQQLGYKTVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASYLQELKSI 229
Db 61 NLGMSQQLGYKTVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASYLQELKSI 120

[1]
QY 230 CKKVEDSQAVDKLVKQVNRKREIEKRGAGIOAAREKNIOKPOENIFLCOALRTFFP 289
Db 121 CKKVEDSQAVDKLVKQVNRKREIEKRGAGIOAAREKNIOKPOENIFLCOALRTFFP 180

QY 290 NSEFLHSCVMSLKNRHSKSSCNYNHLDVVDNLTLMVEHTDIPEASPASTPQIIKHK 347
Db 181 NSEFLHSCVMSLKNRHSKSSCNYNHLDVVDNLTLMVEHTDIPEASPASTPQIIKHK 238

RESULT 3
Q8BT69 PRELIMINARY; PRT; 212 AA.
AC Q8BT69;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN 3830405G04RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Placenta, and Extraembryonic tissue;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK014420; BAC25434.1; -.
DR MGD; MGI:1917931; 3830405G04RIK.
KW Hypothetical protein.
SQ SEQUENCE 212 AA; 24378 MW; 8FA974EE7DDA2AFF CRC64;

Query Match 4.6%; Score 19; DB 11; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 VVGWYKFRHSDQIMTFRE 114
Db 60 VVGWYKFRHSDQIMTFRE 78

RESULT 4
Q8BFV6 PRELIMINARY; PRT; 261 AA.
AC Q8BFV6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN 3830405G04RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK042001; BAC31129.1; -.
DR EMBL; AK042339; BAC31229.1; -.
DR MGD; MGI:1917931; 3830405G04RIK.
KW Hypothetical protein.
SQ SEQUENCE 261 AA; 29688 MW; E87E9CEB73AFE37FF CRC64;

Query Match 4.6%; Score 19; DB 11; Length 261;
Best Local Similarity 100.0%; Pred. No. 5.4e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 VVGWYKFRHSDQIMTFRE 114
DB 96 VVGWYKFRHSDQIMTFRE 114
|||||

RESULT 5
Q8BPZ8 PRELIMINARY; PRT; 407 AA.

ID Q8BPZ8
AC Q8BPZ8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN 3830405G04RIK.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CS7BL/6J; TISSUE-Eye;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK051816; BAC34780.1; -;
DR MGD; MGI:1917931; 3830405G04RIK.
KW Hypothetical protein.
SQ SEQUENCE 407 AA; 46039 MW; FB9B05A197A2B6C4 CRC64;

Query Match 4.6%; Score 19; DB 11; Length 407;
Best Local Similarity 100.0%; Pred. No. 8.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 VVGWYKFRHSDQIMTFRE 114
DB 96 VVGWYKFRHSDQIMTFRE 114
|||||

RESULT 6
Q8K2T7 PRELIMINARY; PRT; 298 AA.

ID Q8K2T7
AC Q8K2T7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to hypothetical protein FLJ13614.
GN 3830405G04RIK.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029845; AAH29845.1; -;
DR MGD; MGI:1917931; 3830405G04RIK.
KW Hypothetical protein.
SQ SEQUENCE 298 AA; 33669 MW; 34CD1CE3AD80B7FB CRC64;

Query Match 3.9%; Score 16; DB 11; Length 298;
Best Local Similarity 100.0%; Pred. No. 8.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 EDGSLKEVHKINEMYA 220
|||||

Db 96 EDGSLKEVHKINEMYA 111
|||||

RESULT 7
Q28405 PRELIMINARY; PRT; 546 AA.

ID Q28405
AC Q28405;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein AF1874.
GN AF1874.

OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VJ-15 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370 (1997).
DR EMBL; AE000973; AAB89382.1; -;
DR PIR; A69484; A69484.
DR TIGR; AF1874; -;
DR GO; GO:0005524; F.ATP binding; IEA.
DR GO; GO:0008026; F.ATP dependent helicase activity; IEA.
DR GO; GO:0003676; F.nucleic acid binding; IEA.
DR InterPro; IPR006474; Cas3_core.
DR InterPro; IPR001410; DEAD_core.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00271; helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICG; 1.
DR TIGRPFAMs; TIGR01587; cas3_core; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 546 AA; 62755 MW; 8A340BD6E1B0D5F3 CRC64;

Query Match 2.2%; Score 9; DB 17; Length 546;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SLOEELKSI 229
DB 62 SLOEELKSI 70
|||||

RESULT 8
Q83R71 PRELIMINARY; PRT; 128 AA.

ID Q83R71
AC Q83R71;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative excisionase.
GN SFI848.

OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;

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RN SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RA MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441(2002).
DR EMBL; AF015204; AAN43409.1; -.
KW Complete proteome.
SQ SEQUENCE 128 AA; 14465 MW; 5C15CF4D34FBD851 CRC64;

Query Match 2.0%; Score 8; DB 16; Length 128;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 ASTPOIHK 345
Db |||||
7 ASTPOIHK 14

RESULT 9
Q8AD48 PRELIMINARY; PRT; 132 AA.
AC Q8AD48;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Gag protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses, Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11876;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97USI.NYP;
RX MEDLINE=22290097; PubMed=12402955;
RA Robbins K.E., Weidle P.J., Brown T.M., Saekhou A.M., Coles B.,
RA Holmberg S.D., Folks T.M., Kalish M.L.;
RT "Molecular Analysis in Support of an Investigation of a Cluster of
RT HIV-1-Infected Women."
RL AIDS Res. Hum. Retroviruses 18:1157-1161(2002).
DR EMBL; AY098617; AAM34529.1; -.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR000071; Retrovir_p17.
DR Pfam; PF00540; Gag_p17; 1.
DR PRINTS; PR00234; HIVIMATRIX.
FT NON_TER 132
SQ SEQUENCE 132 AA; 14713 MW; DC15353302EA07B4 CRC64;

Query Match 2.0%; Score 8; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 ANTGSNNQ 379
Db |||||
120 ANTGSNNQ 127

RESULT 10
Q8YDR8 PRELIMINARY; PRT; 246 AA.
AC Q8YDR8;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Taurine transport system permease protein TAUC.
GN BME10107.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA Delvecchio V.G., Kapatral V., Redkar R.J., Patra G., Mijer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haeckel R., Kyplides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009649; AAL53348.1; -.
DR PIR; AI3522; AI3522.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp; 1.
KW Complete proteome.
SQ SEQUENCE 246 AA; 26410 MW; 23169AF577196634 CRC64;

Query Match 2.0%; Score 8; DB 16; Length 246;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VLSGFVLG 16
Db |||||
63 VLSGFVLG 70

RESULT 11
Q8FUN2 PRELIMINARY; PRT; 250 AA.
AC Q8FUN2;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Taurine ABC transporter, permease protein.
GN BRA1188.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
RA Riedmuller S., Testelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Linder L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts."
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AE014611; AAN34346.1; -.
DR TIGR; BRA1188; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp; 1.
KW Complete proteome.
SQ SEQUENCE 250 AA; 26879 MW; 3EF10C2447568BB0 CRC64;

Query Match 2.0%; Score 8; DB 16; Length 250;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 9 VLSGFVLG 16
DB 63 VLSGFVLG 70

RESULT 12
Q9A4B6 PRELIMINARY; PRT; 297 AA.
AC Q9A4B6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein C2920.
GN C2920.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamachew J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005956; AAK24882.1; -;
DR PIR; F87610; F87610.
DR TIGR; C2920; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 297 AA; 33149 MW; F6ED5CD697B5C0D CRC64;

Query Match 2.0%; Score 8; DB 16; Length 297;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LLGEVKGE 40
DB 267 LLGEVKGE 274

RESULT 13
Q8NCW9 PRELIMINARY; PRT; 301 AA.
AC Q8NCW9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Pfoldin subunit) (Fragment).
GN DKF2P586G0324.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Uterus;
RA Duesterhoef A., Lauber J., Meves H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE PFFOLDIN BETA SUBUNIT FAMILY.
DR EMBL; AL834538; CAD39194.1; -;
DR GO; GO:0003754; F:Chaperone activity; IEA.
DR InterPro; IPR001363; Fetuin.
DR InterPro; IPR002777; PrefoldinK2.
DR Fram; PF01920; K2; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS01255; FETUIN_2; 1.

KW Hypothetical protein; Chaperone.
FT NON_TER 1
SQ SEQUENCE 301 AA; 35048 MW; 4B1E6B92F86CB3D6 CRC64;

Query Match 2.0%; Score 8; DB 4; Length 301;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLQELK 227
DB 76 ASLQELK 83

RESULT 14
Q94401 PRELIMINARY; PRT; 312 AA.
AC Q94401;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative lectin precursor, possible vesicular protein.
GN SPCC126.08C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA Murphy L., Harris D., Lyne M., Rajandream M.A., Barrell B.G.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL034490; CAA22477.1; -;
DR PIR; T40912; T40912.
DR GeneDB SPombe; SPCC126.08c; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR005052; Lectin leg.
DR Pfam; PF03388; Lectin_leg-like; 1.
KW Lectin.
SQ SEQUENCE 312 AA; 35129 MW; F0F17736451ECF82 CRC64;

Query Match 2.0%; Score 8; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GFVLGALA 19
DB 15 GFVLGALA 22

RESULT 15
Q28621 PRELIMINARY; PRT; 322 AA.
AC Q28621;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sarcoplasmic associated protein.
GN SLAP1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Heart;
RA Wigle J.T., Demchyshyn L., Sattar S., Pratt M., Tuana B.S.;
RL "Molecular Cloning of a Novel Family of Sarcoplasmic Associated Coiled-Coil Proteins: Protein-Protein Interactions at the Cell Membrane.";
RT Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.

DR	EMBL; U21155; AAA65598.1; -.
DR	InterPro; IPR001363; FetuIn.
DR	InterPro; IPR002777; PrefoldinKE2.
DR	InterPro; IPR000533; Tropomyosin.
DR	Pfam; PF01920; KE2; 1.
DR	PRINTS; PR00194; TROPOMYOSIN.
DR	PROSITE; PS01255; FETUIN_2; 1.
SQ	SEQUENCE 322 AA; 37410 MW; 8BBC61743860D7A2 CRC64;
Query Match 2.0%; Score 8; DB 6; Length 322;	
Best Local Similarity 100.0%; Pred.No.23;	
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	220 ASLQEELK 227
Dd	
	96 ASLQEELK 103
RESULT 16	
Q9IP73	PRELIMINARY; PRT; 326 AA.
ID	Q9IP73
AC	Q9IP73; (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	VP7.
OS	Human rotavirus G2.
OC	Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX	NCBI_TaxID=73034;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=TW93936;
RA	Lee C.N., Zao C.L.;
RL	Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF044353; AAE74802.1; -.
DR	InterPro; IPR001963; VP7.
DR	Pfam; PF00434; VP7; 1.
DR	ProDom; PD00191; VP7; 1.
SQ	SEQUENCE 326 AA; 37378 MW; B63AG8262A147E6A CRC64;
Query Match 2.0%; Score 8; DB 12; Length 326;	
Best Local Similarity 100.0%; Pred.No.24;	
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	358 KRSLDLT 365
Dd	
	312 KRSLDLT 319
RESULT 17	
Q9H297	PRELIMINARY; PRT; 359 AA.
ID	Q9H297
AC	Q9H297; (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	Sarcolemmal associated protein 1.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Heart;
RA	Wielowieyski P.A., Sevinc S., Guzzo R., Salih M., Wigle J.T.,
RA	Tuana B.S.;
RT	"Alternative Splicing, Expression and Genomic Structure of the 3'
RT	Region of the Gene Encoding the Sarcolemmal Associated Proteins
RT	(SLAP) Defines a Novel Class of Coiled-Coil Tail Anchored Membrane
RT	Proteins."
RL	Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF304450; AAG41949.1; -.
DR	InterPro; IPR001363; FetuIn.

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RT coil proteins: protein-protein interactions at the cell membrane.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U21156; AA65596.1; -.
DR InterPro; IPR001363; Fecuin.
DR InterPro; IPR002777; PrefoldinX2.
DR InterPro; IPR005333; Tropomyosin.
DR Pfam; PF01920; KE2; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS01255; FETUIN 2; 1.
SQ SEQUENCE 402 AA; 46382 MW; F36B1DD852D1DF22 CRC64;

Query Match 2.0%; Score 8; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLQELK 227
Db 176 ASLQELK 183

RESULT 20
Q15018 PRELIMINARY; PRT; 419 AA.
AC Q15018;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein KIAA0157 (Fragment).
GN KIAA0157.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=96127530; PubMed=8590280;
RA Nagase T., Seki N., Tanaka A., Ishikawa K., Nomura N.;
RT Prediction of the coding sequences of unidentified human genes. IV.
RT The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by
RT analysis of cDNA clones from human cell line KG-1."
RL DNA Res. 2:167-174(1995).
RW EMBL; D63877; BAA09927.1; -.
KW Hypothetical protein.
PT NON_TER
SQ SEQUENCE 419 AA; 47368 MW; 50F15AB18BC29D30 CRC64;

Query Match 2.0%; Score 8; DB 4; Length 419;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 EGFLGGEV 37
Db 29 EGFLGGEV 36

RESULT 21
Q8UBL9 PRELIMINARY; PRT; 442 AA.
AC Q8UBL9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE tRNA modification GTPase.
GN THDF OR ATU2832 OR AGR C 5135.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

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RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McLelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Doan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL; AE009230; AAL43813.1; -.
DR EMBL; AE008196; AAK88543.1; -.
DR PIR; AG2924; AG2924.
DR PIR; F97698; F97698.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006400; P:RNA modification; IEA.
DR InterPro; IPR005289; GTP-binding_dom.
DR InterPro; IPR002917; MWR_HSR1.
DR InterPro; IPR005225; Small_GTP.
DR InterPro; IPR004520; ThdF.
DR Pfam; PF01926; MWR_HSR1; 1.
DR TIGRFAMS; TIGR00650; MG442; 1.
DR TIGRFAMS; TIGR00231; small_GTP; 1.
DR TIGRFAMS; TIGR00450; thdF; 1.
KW Complete proteome.
SQ SEQUENCE 442 AA; 47958 MW; 75254C8D0F541CAB CRC64;

Query Match 2.0%; Score 8; DB 16; Length 442;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEKR 257
Db 361 LKREIEKR 368

RESULT 22
Q9Y681 PRELIMINARY; PRT; 452 AA.
AC Q9Y681;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SLAP-2 homolog.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20499367; PubMed=11042152;
RA Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,
RA Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,
RA Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells."
RL Genome Res. 10:1546-1560(2000).
DR EMBL; AF100750; AAB43014.1; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.

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DR GO; GO:0005790; C:smooth endoplasmic reticulum; TAS.
DR GO; GO:0006936; P:muscle contraction; TAS.
DR InterPro; IPR001363; Fetuin.
DR InterPro; IPR002777; PrefoldinKE2.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01920; KE2; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS01255; FETUIN_2; 1.
SQ SEQUENCE 452 AA; 52284 MW; 350581416FD23FCD CRC64;

Query Match          2.0%; Score 8; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLQELK 227
DB 197 ASLQELK 204

RESULT 23
Q9M306 PRELIMINARY; PRT; 470 AA.
AC Q9M306;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN T2J19_30.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
RA Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F.,
RA Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL132963; CAB87904.1; -.
DR PIR; T49272; T49272.
DR InterPro; IPR001594; Znf_DHHC.
DR Pfam; PF01529; zf-DHHC_1.
DR ProDom; PD003041; Znf_DHHC; 1.
DR PROSITE; PS0216; ZF_DHHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 53086 MW; C3300B6FF397344B CRC64;

Query Match          2.0%; Score 8; DB 10; Length 470;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLLT 136
DB 93 DLVFLLLT 100

RESULT 24
Q28623 PRELIMINARY; PRT; 639 AA.
AC Q28623;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sarcolemmal associated protein-3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;

DR GO; GO:0005790; C:smooth endoplasmic reticulum; TAS.
DR GO; GO:0006936; P:muscle contraction; TAS.
DR InterPro; IPR001363; Fetuin.
DR InterPro; IPR002777; PrefoldinKE2.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01920; KE2; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS01255; FETUIN_2; 1.
SQ SEQUENCE 452 AA; 52284 MW; 350581416FD23FCD CRC64;

Query Match          2.0%; Score 8; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLQELK 227
DB 197 ASLQELK 204

RESULT 23
Q9M306 PRELIMINARY; PRT; 470 AA.
AC Q9M306;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN T2J19_30.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
RA Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F.,
RA Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL132963; CAB87904.1; -.
DR PIR; T49272; T49272.
DR InterPro; IPR001594; Znf_DHHC.
DR Pfam; PF01529; zf-DHHC_1.
DR ProDom; PD003041; Znf_DHHC; 1.
DR PROSITE; PS0216; ZF_DHHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 53086 MW; C3300B6FF397344B CRC64;

Query Match          2.0%; Score 8; DB 10; Length 470;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLLT 136
DB 93 DLVFLLLT 100

RESULT 24
Q28623 PRELIMINARY; PRT; 639 AA.
AC Q28623;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sarcolemmal associated protein-3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;

DR GO; GO:0005790; C:smooth endoplasmic reticulum; TAS.
DR GO; GO:0006936; P:muscle contraction; TAS.
DR InterPro; IPR001363; Fetuin.
DR InterPro; IPR002777; PrefoldinKE2.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01920; KE2; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS01255; FETUIN_2; 1.
SQ SEQUENCE 452 AA; 52284 MW; 350581416FD23FCD CRC64;

Query Match          2.0%; Score 8; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLQELK 227
DB 197 ASLQELK 204

RESULT 23
Q9M306 PRELIMINARY; PRT; 470 AA.
AC Q9M306;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN T2J19_30.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
RA Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F.,
RA Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL132963; CAB87904.1; -.
DR PIR; T49272; T49272.
DR InterPro; IPR001594; Znf_DHHC.
DR Pfam; PF01529; zf-DHHC_1.
DR ProDom; PD003041; Znf_DHHC; 1.
DR PROSITE; PS0216; ZF_DHHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 53086 MW; C3300B6FF397344B CRC64;

Query Match          2.0%; Score 8; DB 10; Length 470;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLLT 136
DB 93 DLVFLLLT 100

RESULT 24
Q28623 PRELIMINARY; PRT; 639 AA.
AC Q28623;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sarcolemmal associated protein-3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;

DR GO; GO:0005790; C:smooth endoplasmic reticulum; TAS.
DR GO; GO:0006936; P:muscle contraction; TAS.
DR InterPro; IPR001363; Fetuin.
DR InterPro; IPR002777; PrefoldinKE2.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01920; KE2; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS01255; FETUIN_2; 1.
SQ SEQUENCE 452 AA; 52284 MW; 350581416FD23FCD CRC64;

Query Match          2.0%; Score 8; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLQELK 227
DB 197 ASLQELK 204

RESULT 23
Q9M306 PRELIMINARY; PRT; 470 AA.
AC Q9M306;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN T2J19_30.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
RA Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F.,
RA Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL132963; CAB87904.1; -.
DR PIR; T49272; T49272.
DR InterPro; IPR001594; Znf_DHHC.
DR Pfam; PF01529; zf-DHHC_1.
DR ProDom; PD003041; Znf_DHHC; 1.
DR PROSITE; PS0216; ZF_DHHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 53086 MW; C3300B6FF397344B CRC64;

Query Match          2.0%; Score 8; DB 10; Length 470;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLLT 136
DB 93 DLVFLLLT 100

RESULT 24
Q28623 PRELIMINARY; PRT; 639 AA.
AC Q28623;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sarcolemmal associated protein-3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
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DT 01-WAR-2003 (TREMBLrel. 23, Created)
DT 01-WAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-WAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN AT3G23590/MDBI9.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosida II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RC Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RC Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RA "Arabidopsis thaliana full-length cDNA.";
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK117119; BAC41797.1; -.
RD Hypothetical protein.
KW SEQUENCE
SQ SEQUENCE 1309 AA; 143067 MW; F569651F17C287C1 CRC64;

Query Match 2.0%; Score 8; DB 10; Length 1309;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 VPLVWNL 171
DB 404 VPLVWNL 411
|||||

RESULT 29
P72388 PRELIMINARY; PRT; 81 AA.
ID P72388
AC P72388;
DT 01-PFB-1997 (TREMBLrel. 02, Created)
DT 01-PFB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Transposase (Fragment).
DE Staphylococcus aureus.
OS Bacteria; Firmicutes; Bacillales; Staphylococcus.
OC NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC Mananara P.M., Landolo J.J.;
RC TRANSPOSON-Tn51;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75367; AAB18959.1; -.
DR InterPro; IPR002513; Transposase_7.
DR Pfam; PF01526; Transposase_7; 1.
FT NON_TER 1
FT NON_TER 81
FT NON_TER 81
SQ SEQUENCE 81 AA; 9490 MW; B957359583F72C12 CRC64;

Query Match 1.7%; Score 7; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 SICKKVE 234
DB 4 SICKKVE 10
|||||

RESULT 30
Q90A88 PRELIMINARY; PRT; 88 AA.
ID Q90A88
AC Q90A88;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.

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OX Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=622393;
RA Op de Coul E.L.M., Coutinho R.A., van der Schoot A.,
van Doornum G.J.J., Lukashov V.V., Goudsmit J., Cornelissen M.;
"The impact of immigration on the env HIV-1 subtype distribution among
heterosexuals in the Netherlands: influx of subtype B and non-B
strains"; (2001).
RL AIDS 0:0-0(2001).
DR EMBL; AF403886; AAL05694.1; --
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1 1
FT NON_TER 88 88
SQ SEQUENCE 88 AA; 9862 MW; D7F9DDCF0CC39033 CRC64;

Query Match 1.7%; Score 7; DB 15; Length 88;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 LQEHFSN 127
Db 79 LQEHFSN 85
|||||

RESULT 31
Q9DR26 PRELIMINARY; PRT; 88 AA.
AC Q9DR26;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DD96061;
RX MEDLINE=21002580; PubMed=11118076;
RA Abebe A., Pollakis G., Fontanet A.L., Fisseha B., Tegbaru B.,
Kliphuis A., Tesfaye G., Negassa H., Cornelissen M., Goudsmit J.,
Rinke de Wit T.F.;
"Identification of a genetic sub-cluster of HIV-1 subtype C (C')
widespread in Ethiopia";
RL AIDS Res. Hum. Retroviruses 16:1909-1914(2000).
DR EMBL; AF245566; AAG40679.1; --
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1 1
FT NON_TER 88 88
SQ SEQUENCE 88 AA; 9912 MW; 7377D7552CB203B9 CRC64;

Query Match 1.7%; Score 7; DB 15; Length 88;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 LQEHFSN 127
Db 79 LQEHFSN 85
|||||

RESULT 32
Q90BJ1 PRELIMINARY; PRT; 91 AA.
AC Q90BJ1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=seroconverter-B;
RA Rinke de Wit T.F., Tsegaye A., Wolday D., Hailu B., Aklilu M.,
Sanders E., Hagos W., Kliphuis A., Pollakis G., Krol A., Gesskus R.,
Miedema F., Goudsmit J., Coutinho R.A., Fontanet A.L.;
"Particulars of HIV-1 subtype C primary infection in Ethiopia";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF391828; AAL06743.1; --
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1 1
FT NON_TER 91 91
SQ SEQUENCE 91 AA; 10325 MW; 81E9B71E38942BC9 CRC64;

Query Match 1.7%; Score 7; DB 15; Length 91;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 LQEHFSN 127
Db 79 LQEHFSN 85
|||||

RESULT 33
Q9KF07 PRELIMINARY; PRT; 92 AA.
AC Q9KF07;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein BH0692.
GN BH0692.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
"Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001509; BAB04411.1; --
DR PIR; D83736; D83736.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 92 AA; 10704 MW; AA259398DDC6A1B CRC64;

Query Match 1.7%; Score 7; DB 16; Length 92;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 ERLHKN 120
|||||

Query Match	1.7%	Score 7	DB 10	Length 100
Best Local Similarity	100.0%	Pred. No. 93		
Matches 7; Conservative	0	Mismatches 0	Indels 0	Gaps 0
DE	Emb CAB39646.1.	OS	Arabisopsis thaliana (Mouse-ear cress)	
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids;			

eurosid II; Brassicales; Brassicaceae; Arabidopsis.
ID NCBI_TaxID=3702;
AC Q8XGT8 PRELIMINARY; PRT; 105 AA.
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE SUGe protein (Putative DMT superfamily transport protein).
GN SUGe OR T4390 OR STM4338 OR STY4699.
OS Salmonella typhi, and
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601, 602;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;
RA "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18";
RL J. Bacteriol. 185:2330-2337(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2";
RL Nature 413:852-856(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Comerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RA "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18";
RL Nature 413:848-852(2001).
DR EMBL; AF0016849; AAC071841.1; -;
DR EMBL; AF0008903; AAL23161.1; -;
DR EMBL; AL627283; CAD06818.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000390; Smr.
DR Pfam; PF00893; Multi_Drug_Res; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 105 AA; 10869 MW; 1D396AF413953701 CRC64;
Query Match 1.7%; Score 7; DB 16; Length 105;
Best Local Similarity 100.0%; Pred.No. 97;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 135 LTPSIIT 141
DB 29 LTPSIIT 35
RESULT 39
Q9LWQO PRELIMINARY; PRT; 108 AA.
AC Q9LWQO;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
Q8XGT8

eurosid II; Brassicales; Brassicaceae; Arabidopsis.
ID NCBI_TaxID=3702;
AC Q82IX9 PRELIMINARY; PRT; 104 AA.
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Putative chaparrone.
GN SUGe OR YPO0355.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
RA "Genome sequence of Yersinia pestis, the causative agent of plague";
RL Nature 413:523-527(2001).
DR EMBL; AJ414142; CAC89214.1; -;
DR PIR; AC0044; AC0044.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000390; Smr.
DR Pfam; PF00893; Multi_Drug_Res; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 104 AA; 10651 MW; 6DADB41E0B97B5B8 CRC64;
Query Match 1.7%; Score 7; DB 16; Length 104;
Best Local Similarity 100.0%; Pred.No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 135 LTPSIIT 141
DB 29 LTPSIIT 35
RESULT 38
Q8XGT8

DE EST AU065411(R3610) corresponds to a region of the predicted gene
DE (P0489A05.29 protein).
GN P0489A05.29.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone:P0451C06.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone:P0489A05.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP001551; BAA92945.1; -;
DR EMBL; AP003105; BAB33006.1; -;
DR Gramene; Q9LWQ0; -;
SQ SEQUENCE 108 AA; 10846 MW; 1768BA3625B367D0 CRC64;

Query Match 1.7%; Score 7; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LVFLLLT 136
DB 13 LVFLLLT 19

RESULT 40
Q8E6E9 PRELIMINARY; PRT; 110 AA.
AC Q8E6E9;
DT 01-WAR-2003 (TREMBLrel. 23, Created)
DT 01-WAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN GBS0619.
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OX NCBI_TaxID=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaser P., Rusnick C., Buchrieser C., Chevalier F., Frangeul L.,
RA Msadek T., Zouine M., Couve E., Lalicui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513 (2002).
DR EMBL; AL766846; CAD46263.1; -;
DR Sgallist; gbs0619; -;
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR005877; Gpos_YsIRK.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 110 AA; 11790 MW; A646631D04201ADF CRC64;

Query Match 1.7%; Score 7; DB 16; Length 110;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 STSAVLS 11

DB 84 STSAVLS 90
|||||
RESULT 41
Q8A302 PRELIMINARY; PRT; 114 AA.
AC Q8A302;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN BT3153
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 291148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076 (2003).
DR EMBL; AB016939; AAO78259.1; -;
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001387; HTH_3.
DR Pfam; PF01381; HTH_3; 1.
DR SMART; SM00530; HTH_XRE; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 114 AA; 13497 MW; 1D123D55E0F9EF18 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 114;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KDVNRLK 251
DB 47 KDVNRLK 53
|||||
RESULT 42
Q7ZEP5 PRELIMINARY; PRT; 115 AA.
AC Q7ZEP5;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=02timene1019;
RA Subtuent K.;
RT "Molecular Epidemiology of HIV-1 in Thailand.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY248086; AAP14146.1; -;
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 115
SQ SEQUENCE 115 AA; 13100 MW; 1188484FA395449B CRC64;

Query Match 1.7%; Score 7; DB 15; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 LQEHFSN 127

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DB 73 LQEHFSN 79
|||||
RESULT 43
Q8V6V7 PRELIMINARY; PRT; 116 AA.
AC Q8V6V7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Halovirus HF2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=33771;
RN [1]
RP SEQUENCE FROM N.A.
RA Tang S.-L., Fisher C., Ngui K., Nuttall S.D., Dyal-Smith M.L.;
RT "Sequence and transcription of halovirus HF2.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF222060; AAL54923.1; -.
KW Hypothetical protein.
SQ SEQUENCE 116 AA; 13646 MW; EA69EC3F77FFA37A CRC64;

Query Match 1.7%; Score 7; DB 12; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEK 396
|||||
DB 88 TDEIEK 94

RESULT 44
Q7TDP0 PRELIMINARY; PRT; 116 AA.
AC Q7TDP0;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Halovirus HF1.
OC Viruses; unclassified viruses; Haloviruses.
OX NCBI_TaxID=222645;
RN [1]
RP SEQUENCE FROM N.A.
RA Tang S.-L., Nuttall S.D., Dyal-Smith M.L.;
RT "Nucleotide sequence of halovirus HF1: close similarity to HF2 and evidence for a recent and large recombination event.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY190604; AAO61301.1; -.
KW Hypothetical protein.
SQ SEQUENCE 116 AA; 13646 MW; EA69EC3F77FFA37A CRC64;

Query Match 1.7%; Score 7; DB 12; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEK 396
|||||
DB 88 TDEIEK 94

RESULT 45
Q8Y4K1 PRELIMINARY; PRT; 136 AA.
AC Q8Y4K1;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical protein lmo2437.
OS Listeria monocytogenes.

Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Baquero F., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Charbit A., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Domann E., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Entian K.-D., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Gautier L., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkak G.,
RA Jones L.-M., Matounam A., Mata Vicente J., Ng B., Nedjari H.,
RA Madueno E., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Madsen E., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Remmel B., Voss H., Weiland J., Cossart P.;
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591983; CAD00515.1; -.
DR PIR; A81379; A81379.
DR Listlist; LMO2437; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 136 AA; 15676 MW; 75B479CEA21F899B CRC64;

Query Match 1.7%; Score 7; DB 16; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 QAVDKLV 244
|||||
DB 86 QAVDKLV 92

RESULT 46
Q9UZRS PRELIMINARY; PRT; 136 AA.
AC Q9UZRS;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical protein PYRAB10800.
GN PYRAB10800 OR PAB0720.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GES / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ248286; CAB49991.1; -.
DR PIR; B75086; B75086.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 136 AA; 15404 MW; 6920B94FD72B6917 CRC64;

Query Match 1.7%; Score 7; DB 17; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 EEIEKMK 398
|||||
DB 98 EEIEKMK 104

RESULT 47
Q8UIN2 PRELIMINARY; PRT; 137 AA.
AC Q8UIN2;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
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DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GN Hypothetical protein PF1174.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF010226; AAL51298.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 137 AA; 15687 MW; 4BFC98EA2E986FD1 CRC64;

Query Match 1.7%; Score 7; DB 17; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 EEIERMK 398
Db 98 EEIERMK 104

RESULT 48
ID Q93MB9 PRELIMINARY; PRT; 138 AA.
AC Q93MB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PCP28.
GN PCP28.
OS Clostridium perfringens.
OG Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AF003515; BAB62466.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR005357; UPF0150.
DR Pfam; PF03681; UPF0150; 1.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 138 AA; 15675 MW; 64B4C0FA6ED901E2 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 138;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 ETDEEIE 395
Db 56 ETDEEIE 62

RESULT 49
ID Q9XX55 PRELIMINARY; PRT; 140 AA.
AC Q9XX55;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
```

```
DE Y38H6C.3 protein.
GN Y38H6C.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA White S.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AL031630; CAA20983.1; -.
DR FIR; T26693; T26693.
DR WormPep; Y38H6C.3; CE19097.
SQ SEQUENCE 140 AA; 16445 MW; AEDC919D930D6B58 CRC64;

Query Match 1.7%; Score 7; DB 5; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 REIEKER 258
Db 44 REIEKER 50

RESULT 50
ID Q93SS4 PRELIMINARY; PRT; 143 AA.
AC Q93SS4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Exbd.
GN Exbd.
OS Plesiomonas shigelloides (Aeromonas shigelloides).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Plesiomonas.
OX NCBI_TaxID=703;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21189295; PubMed=11292789;
RA Henderson D.P., Wyckoff E.E., Rashidi C.E., Verlei H., Oldham A.L.;
RT "Characterization of the Plesiomonas shigelloides genes encoding the
RT Heme Iron Utilization System."
RL J. Bacteriol. 183:2715-2723(2001).
DR EMBL; AY008342; AAG23398.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003400; Exbd.
DR Pfam; PF02472; Exbd; 1.
SQ SEQUENCE 143 AA; 15711 MW; E713E9FF1FD1088A CRC64;

Query Match 1.7%; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LVFILLT 136
Db 28 LVFILLT 34

RESULT 51
ID Q89F14 PRELIMINARY; PRT; 144 AA.
AC Q89F14;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
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DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE B1r6887 protein.
GN B1r6887.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idegawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005960; BAC52152.1; -.
KW Complete proteome.
SQ SEQUENCE 144 AA; 15281 MW; 924ABDEBF76679F8 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 TGFGRV 195
DB 28 TGFGRV 34
|||||

RESULT 52
Q8EB62 PRELIMINARY; PRT; 145 AA.
AC Q8EB62;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-JUN-2003 (TrEMBLrel. 23, Last sequence update)
DE TonB system transport protein ExbD1.
GN ExbD1 OR SO3672.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vanatavan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Neallson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015802; AAN56657.1; -.
DR TIGR; SO3672; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003400; ExbD.
DR Pfam; PF02472; ExbD; 1.
KW Complete proteome.
SQ SEQUENCE 145 AA; 15477 MW; 7920728490CF7219 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLL 135
DB 97 DLVFLLL 103
|||||

RESULT 54
Q8UIG7 PRELIMINARY; PRT; 153 AA.
AC Q8UIG7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nitrogen regulatory IIA protein.
GN PISN OR ATU0330 OR AGR_C576.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Chena V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Kura Y., Paulsen I.T., Bisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmeri A., Gordon D.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liac I., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Humbley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
RA Qurollo B., Goldman B.S., Gao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR EMBL; AE009004; AAL4352.1; -.
DR EMBL; AE007971; AAK86147.1; -.
DR PIR; AB2617; AB2617.
DR PIR; B97399; B97399.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006320; PtsN_nitro_regn.
DR InterPro; IPR002178; Pts_EIIA_2.
DR Pfam; PF00359; Pts_EIIA_2; 1.
DR ProDom; PD001689; Pts_EIIA_2; 1.
DR TIGRfams; TIGR01419; nitro_reg_IIA; 1.
DR PROSITE; PS00372; Pts_EIIA_2; 1.
KW Complete proteome.
SQ SEQUENCE 153 AA; 16470 MW; EF28EB87ADA99450 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Q8D1E4
ID Q8D1E4 PRELIMINARY; PRT; 153 AA.
AC Q8D1E4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Suppresses groEL, may be chaparone.
SUGS OR Y0613.
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RC MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Versinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AE013663; AAM84201.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000390; Smr.
DR Pfam; PF00893; Multi_Drug_Res; 1.
SQ SEQUENCE 153 AA; 16153 MW; FFE92A5044FBF195 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 LTPSIIT 141
DB 78 LTPSIIT 84

RESULT 55
Q98GS7
ID Q98GS7 PRELIMINARY; PRT; 154 AA.
AC Q98GS7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phosphotransferase system enzyme II (EC 2.7.1.69).
GN MLL3194.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RC MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AF003001; BAB50139.1; -;
DR GO; GO:0008982; F:protein-N(Pi)-phosphohistidine-sugar phospho. .; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008401; P:phosphoenolpyruvate-dependent sugar phospho. .; IEA.
DR GO; GO:0008810; P:transport; IEA.
DR InterPro; IPR006320; Ptsn_nitro_regn.
DR InterPro; IPR002178; Pts_EIIA_2.
DR Pfam; PF00359; Pts_EIIA_2; 1.
DR ProDom; PD001689; Pts_EIIA_2; 1.

Q98GS7
ID Q98GS7 PRELIMINARY; PRT; 154 AA.
AC Q98GS7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Probable nitrogen regulatory IIA protein (EC 2.7.1.69).
GN Ptsn OR R00379 OR SMC01141.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RC MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boissard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelie D., Puhler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Gallibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591783; CAC41816.1; -;
DR GO; GO:0008982; F:protein-N(Pi)-phosphohistidine-sugar phospho. .; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006320; Ptsn_nitro_regn.
DR InterPro; IPR002178; Pts_EIIA_2.
DR Pfam; PF00359; Pts_EIIA_2; 1.
DR ProDom; PD001689; Pts_EIIA_2; 1.
DR TIGRFAMs; TIGR01419; nitro_reg_IIA; 1.
DR PROSITE; PS00372; Pts_EIIA_2; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 154 AA; 16438 MW; 79BEB44F78BE9462 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLL 135
DB 97 DLVFLLL 103

RESULT 57
Q8YEUI
ID Q8YEUI PRELIMINARY; PRT; 154 AA.
AC Q8YEUI;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nitrogen regulatory IIA protein (EC 2.7.1.69).
GN BME1786.
OS Brucella melitensis.
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DR TIGRFAMs; TIGR01419; nitro_reg_IIA; 1.
DR PROSITE; PS00372; Pts_EIIA_2; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 154 AA; 16302 MW; AE8B5B5EB30301EC CRC64;

Query Match 1.7%; Score 7; DB 16; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLL 135
DB 97 DLVFLLL 103

RESULT 56
Q92SJ9
ID Q92SJ9 PRELIMINARY; PRT; 154 AA.
AC Q92SJ9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Probable nitrogen regulatory IIA protein (EC 2.7.1.69).
GN Ptsn OR R00379 OR SMC01141.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RC MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boissard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelie D., Puhler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Gallibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591783; CAC41816.1; -;
DR GO; GO:0008982; F:protein-N(Pi)-phosphohistidine-sugar phospho. .; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006320; Ptsn_nitro_regn.
DR InterPro; IPR002178; Pts_EIIA_2.
DR Pfam; PF00359; Pts_EIIA_2; 1.
DR ProDom; PD001689; Pts_EIIA_2; 1.
DR TIGRFAMs; TIGR01419; nitro_reg_IIA; 1.
DR PROSITE; PS00372; Pts_EIIA_2; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 154 AA; 16438 MW; 79BEB44F78BE9462 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLL 135
DB 97 DLVFLLL 103

RESULT 57
Q8YEUI
ID Q8YEUI PRELIMINARY; PRT; 154 AA.
AC Q8YEUI;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nitrogen regulatory IIA protein (EC 2.7.1.69).
GN BME1786.
OS Brucella melitensis.
```

DR	Pfam; PF00359; PTS_EIIA_2; 1.	
DR	ProDom; P001689; PTS_EIIA_2; 1.	
DR	TIGRFamS; TIGR01419; nitro_reg_IIA; 1.	
DR	DR PROSITE; PS00372; PTS_EIIA_2; 1.	
KW	Complete proteome.	
SQ	SEQUENCE 154 AA; 16467 MW; DFE530086D685CB4 CRC64;	
Query Match 1.7%; Score 7; DB 16; Length 154;		
Best Local Similarity 100.0%; Pred. No. 1.4e+02;		
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	129 DIVFLL 135	
DB	97 DIVFLL 103	
RESULT 59		
ID	Q9AKF2 PRELIMINARY; PRT; 155 AA.	
AC	Q9AKF2;	
DT	01-JUN-2001 (TrEMBLrel. 17, Created)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Hypothetical protein.	
OS	Rickettsia rickettsii.	
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;	
OC	Rickettsiaceae; Rickettsiae; Rickettsia.	
CC	NCBI_TaxID=783;	
CC	[1]_SEQUENCE FROM N.A.	
RP	STRAIN=84-21C;	
RC	MEDLINE=21219194; PubMed=11319266;	
RX	Andersson J.O.; Andersson S.G.E.;	
RT	"Pseudogenes, junk DNA and the dynamics of Rickettsia genomes.";	
RL	Mol. Biol. Evol. 18:829-839(2001).	
RT	EMBL; AJ293329; CAC3713.1; --	
KW	Hypothetical protein.	
SQ	SEQUENCE 155 AA; 17335 MW; C7FC8DC4948E288B CRC64;	
Query Match 1.7%; Score 7; DB 2; Length 155;		
Best Local Similarity 100.0%; Pred. No. 1.4e+02;		
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	133 LLTFSI 139	
DB	14 LLTFSI 20	
RESULT 60		
ID	Q9LIZ1 PRELIMINARY; PRT; 156 AA.	
AC	Q9LIZ1;	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)	
DE	Hypothetical protein.	
OS	Oryza sativa (Rice).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
OC	Znariaceae; Oryzaceae; Oryza.	
CC	NCBI_TaxID=4350;	
CC	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=cv. Nipponbare;	
RT	Sasaki T.; Matsumoto T.; Yamamoto K.;	
RT	"Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC	
RT	clone: P0693B08.";	
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBSJ databases.	
EMBL	AF001081; EAA9382.1; --	
DR	DR Gramine; O9LIZ1; --	
KW	Hypothetical protein.	
SQ	SEQUENCE 156 AA; 16354 MW; CE094FAE763290EE CRC64;	

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Query Match 1.7%; Score 7; DB 10; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 STGFSRA 194
DB 98 STGFSRA 104

RESULT 61
Q9RN96 PRELIMINARY; PRT; 158 AA.
AC Q9RN96
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE M protein precursor (Fragment).
GN EMM.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NS292;
RA Bessen D.E.; Carapetis J.R.; Beall B.; Katz R.; Hibble M.;
RA Currie B.J.; Collingridge T.; Izzo M.W.; Scaramuzzino D.A.;
RA Sriprakash K.S.;
RT "Contrasting Molecular Epidemiology of Group A Streptococci Causing
RT Tropical and Non-Tropical Infections.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RW EMBL; AF193966; AAD55745.1; -
KW Signal
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >158 M PROTEIN.
FT NON_TER 158 158
SQ SEQUENCE 158 AA; 17948 MW; 7C2193A1DF6FE51C CRC64;

Query Match 1.7%; Score 7; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KREIEKR 257
DB 148 KREIEKR 154

RESULT 62
Q94UY8 PRELIMINARY; PRT; 173 AA.
AC Q94UY8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit 6.
OS Pluvialis squatarola (Black-bellied plover).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Charadriiformes; Charadriidae;
OC Pluvialis.
OX NCBI_TaxID=171273;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen X.-F.; Li Q.-W.;
RT "Studies on the phylogenetic relationship among 14 species of
RT Charadriiformes from the complete mitochondrial NADH dehydrogenase
RT subunit 6 (ND6) gene.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RW EMBL; AF411399; AAL29218.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
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DR InterPro; IPR001457; Oxidored_q3.
DR Pfam; PF00499; oxidored_q3; 1.
KW Mitochondrion.
SQ SEQUENCE 173 AA; 18073 MW; 7E35C3692D8E7D31 CRC64;

Query Match 1.7%; Score 7; DB 8; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FVLGALA 19
DB 12 FVLGALA 18

RESULT 63
Q958D2 PRELIMINARY; PRT; 173 AA.
ID Q958D2
AC Q958D2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit VI.
OS Tinamus major (Great tinamou).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Palaeognathae; Tinamiformes; Tinamidae; Tinamus.
OX NCBI_TaxID=30468;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21263106; PubMed=11370967;
RA Haddath O.; Baker A.J.;
RT "Complete mitochondrial DNA genome sequences of extinct birds: ratite
RT phylogenetics and the vicariance biogeography hypothesis.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:939-945(2001).
DR EMBL; AF338707; AAK53254.1; -
DR PIR; E90621; E90621.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR001457; Oxidored_q3.
DR Pfam; PF00499; oxidored_q3; 1.
KW Mitochondrion.
SQ SEQUENCE 173 AA; 18293 MW; D56C94812DD14F4A CRC64;

Query Match 1.7%; Score 7; DB 8; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FVLGALA 19
DB 12 FVLGALA 18

RESULT 64
Q958A8 PRELIMINARY; PRT; 174 AA.
ID Q958A8
AC Q958A8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit VI.
OS Pterocnemia pennata (Lesser rhea) (Darwin's rhea).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Palaeognathae; Rheiformes; Rheidae; Pterocnemia.
OX NCBI_TaxID=8795;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21263106; PubMed=11370967;
RA Haddath O.; Baker A.J.;
RT "Complete mitochondrial DNA genome sequences of extinct birds: ratite
RT phylogenetics and the vicariance biogeography hypothesis.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:939-945(2001).
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RN  SEQUENCE FROM N.A.
RP  Haddath O., Baker A.J.;
RA  Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RL  EMBL; AF338709; AAK53280.1; -.
RM  PIR; E90617; E90617.
DR  GO; GO:0005739; C:mitochondrion; IEA.
DR  GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR  GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR  InterPro; IPR001457; Oxidored_g3.
DR  Pfam; PF00499; Oxidored_g3; 1.
KW  Mitochondrion.
SQ  SEQUENCE 174 AA; 18296 MW; 51B6C82E6CA22746 CRC64;

Query Match 1.7%; Score 7; DB 8; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FVLGALA 19
DB 13 FVLGALA 19
|||||

RESULT 65
O57255 PRELIMINARY; PRT; 177 AA.
AC O57255;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative 20.7k protein.
GN MVAL75R.
OS Vaccinia virus (strain Ankara).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=126794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ankara;
RA Antoine G., Scheiflinger F., Falkner F.G., Dörner F.;
RT "The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain.";
RL EMBL; U94848; AAB96549.1; -.
DR PIR; T37444; T37444.
SQ SEQUENCE 177 AA; 20732 MW; 5033B53EB73979E6 CRC64;

Query Match 1.7%; Score 7; DB 12; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 SIITESC 144
DB 62 SIITESC 68
|||||

RESULT 66
O8QMP4 PRELIMINARY; PRT; 181 AA.
AC O8QMP4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE V192.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RX MEDLINE=83117629; PubMed=6961398;
RA Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;
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RT "Sequence of terminal regions of cowpox virus DNA: arrangement of
repeated and unique sequence elements.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RX MEDLINE=90177240; PubMed=2309453;
RA Parsons B.L., Pickup D.J.;
RT "Transcription of orthopoxvirus telomeres at late times during
infection.";
RL Virology 175:69-80(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RX MEDLINE=91196263; PubMed=2014645;
RA Hu F.Q., Pickup D.J.;
RT "Transcription of the terminal loop region of vaccinia virus DNA is
initiated from the telomere sequences directing DNA resolution.";
RL Virology 181:716-720(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RX MEDLINE=94378510; PubMed=8091665;
RA Hu F.Q., Smith C.A., Pickup D.J.;
RT "Cowpox virus contains two copies of an early gene encoding a soluble
secreted form of the type II TNF receptor.";
RL Virology 204:343-356(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RA Pickup D.J.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RA Dietrich F.S., Ray C.A., Sharma A.D., Allen A., Pickup D.J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF482758; AAM13640.1; -.
SQ SEQUENCE 181 AA; 21169 MW; 35E8A36E26A89D45 CRC64;

Query Match 1.7%; Score 7; DB 12; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 SIITESC 144
DB 61 SIITESC 67
|||||

RESULT 67
O9JFT2 PRELIMINARY; PRT; 181 AA.
AC O9JFT2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE C3R.
OS Ectromelia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=12643;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Moscow;
RX MEDLINE=20192152; PubMed=10725549;
RA Chen N., Buller R.M.L., Wall E.M., Upton C.;
RT "Analysis of host response modifier ORFs of ectromelia virus, the
causative agent of mousepox.";
RL Virus Res. 66:155-173(2000).
DR EMBL; AF012825; AAC9562.1; -.
SQ SEQUENCE 181 AA; 21184 MW; 727B5DC1B1D8C927 CRC64;
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Query Match 1.7%; Score 7; DB 12; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 SIITESC 144
Db 61 SIITESC 67

RESULT 69
Q8V4S0 PRELIMINARY; PRT; 181 AA.
AC Q8V4S0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Predicted phosphoesterase.
GN TTE0681.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=2192816; PubMed=1197336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; A2013036; AAM23945.1; -;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004843; M:peptidase.
DR InterPro; IPR000979; UPF0025.
DR Pfam; PF00149; Metallophos; 1.
DR TIGRFAMs; TIGR00040; yfcs; 1.
KW Complete proteome.
SQ SEQUENCE 181 AA; 20412 MW; DE45021A081FED6D CRC64;

Query Match 1.7%; Score 7; DB 16; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEK 396
Db 106 TDEIEK 112

RESULT 69
Q8V4S0 PRELIMINARY; PRT; 182 AA.
AC Q8V4S0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE BBR.
GN BBR.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Zaire-96-I-16;
RX MEDLINE=2159287; PubMed=11734207;
RA Shchelkunov S.N., Totmenin A.V., Babkin I.V., Safronov P.F.,
Ryazankina O.I., Petrov N.A., Gutorov V.V., Uvarova E.A.,
Mikheev M.V., Sisler J.R., Eposito J.J., Jahrling P.B., Moss B.,
Sandakhchiev L.S.;
RT "Human monkeypox and smallpox viruses: genomic comparison.";
RL FEBS Lett. 509:66-70(2001).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=Zaire-96-I-16;
RA Shchelkunov S.N., Totmenin A.V., Safronov P.F., Gutorov V.V.,
Ryazankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A.,
Eposito J.J., Moss B., Sisler J.R., Jahrling P.B., Sandakhchiev L.S.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF380138; AAL40627.1; -;
SQ SEQUENCE 182 AA; 21488 MW; E248F33C227DC77C CRC64;

Query Match 1.7%; Score 7; DB 12; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 SIITESC 144
Db 62 SIITESC 68

RESULT 70
Q9WGAL PRELIMINARY; PRT; 182 AA.
AC Q9WGAL;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 21.3K protein (TB7R).
GN B7R.
OS Vaccinia virus (strain Tian Tan), and
OS Vaccinia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10253; 10245;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Vaccinis virus; STRAIN=PRAHA;
RA Stoller V., Ludvikova V., Maresova L., Nemeckova S., Vonka V.;
RT "Effect of interferon gamma receptor gene deletion on Vaccinia virus
virulence.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TIAN TAN;
RA Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang X.K.,
Jin Q., Hou Y.D., Yuan J.S., Ma X.J.;
RA Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;
RT "Complete genomic sequence of vaccinia virus (Tian Tan strain).";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF120160; AAD22049.1; -;
DR EMBL; AF095689; AAF34076.1; -;
SQ SEQUENCE 182 AA; 21298 MW; 955DF62A1EEE6981 CRC64;

Query Match 1.7%; Score 7; DB 12; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 SIITESC 144
Db 62 SIITESC 68

RESULT 71
O72743 PRELIMINARY; PRT; 182 AA.
AC O72743;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE B6R protein.
GN B6R.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RX MEDLINE=97068532; PubMed=8963248;
RA Saifonov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V.,
RA Shchelkunov S.N., Sandakchiev L.S.;
RT "Genes of a circle of hosts for the cowpox virus.";
RL Dokl. Akad. Nauk 349:829-833(1996).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RA Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Mihaev M.V.,
RA Ryzankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.U.,
RA Sandakchiev L.S.;
RT "Structure-function and organization of cowpox virus strain GRI-90
complete genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RA Totmenin A.V.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; X94355; CAD90732.1; -;
SQ SEQUENCE 182 AA; 21274 MW; 42BA561C312B757E CRC64;

Query Match 1.7%; Score 7; DB 12; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 SIITESC 144
DB 62 SIITESC 68
[1]|||||
[2]
ID 022194 PRELIMINARY; PRT; 185 AA.
AC 022194;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative proline-rich protein (Arabinogalactan protein AGP17).
GN T20D16.24 OR AT2G23130.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid1; Brassicales; Brassicaceae; Arabidopsi1.
OX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Gilson P., Gaspar Y.M., Oxley D., Youl J.J., Bacic A.;
RT "NaCP4 is an arabinogalactan protein whose expression is suppressed
by wounding and fungal infection in Nicotiana glauca.";
RL Protoplasma 0:0-0(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]

RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Trukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
annotation.";
RL Genome Biol. 0:0-0(2002).
[7]
RP SEQUENCE FROM N.A.
RA Brover V., Trukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
[8]
RP SEQUENCE FROM N.A.
RA Yanada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Arabidopsis Full length cDNA Clones.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
[9]
RP SEQUENCE FROM N.A.
RA Yanada K., Dale J.M., Hsuan V.W., Onodera C.S., Quach H.L., Chen H.,
RA Toriumi M., Wong C., Wu H.C., Yu G., Yuan S., Carninci P., Chen H.,
RA Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Kawai J.,
RA Kim C.J., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Tripp M.G., Wu T., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002391; AAB87117.1; -;
DR EMBL; AF030539; AAG41563.1; -;
DR EMBL; AC004401; AAM14931.1; -;
DR EMBL; AY086875; AAM63921.1; -;
DR EMBL; BT002926; AAC22741.1; -;
DR EMBL; BT008601; AAP40426.1; -;
DR PIR; T00519; T00519.
SQ SEQUENCE 185 AA; 18481 MW; 64A10CD28BF8EBAC CRC64;

Query Match 1.7%; Score 7; DB 10; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 PASTPQI 343
DB 76 PASTPQI 82
[1]|||||
[2]
RESULT 73
P93674 PRELIMINARY; PRT; 187 AA.
ID P93674;
AC P93674;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative 21kD protein precursor.
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid1; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX NCBI_TaxID=3879;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=A2; Tissue=Node; Ratet P.;
RA Coronado C., Ratet P.;

Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL: Y11553; CAA72315.1; -
DR PIR: T09390; T09390.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0005225; F:transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR007186; PME1.
DR InterPro: IPR006501; PME_inhib.
DR Pfam: PF04043; PME1; 1.
DR TIGRFAMs: TIGR01614; PME_inhib; 1.
DR PROSITE: PS00430; TONE_DEPENDENT_REC_1; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 187 AA; 20639 MW; BF60799E3166DFB5 CRC64;
1 18
POTENTIAL.
Query Match
Best Local Similarity 1.7%; Score 7; DB 10; Length 187;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 130 LVFLLLT 136
DB 7 LVFLLLT 13
RESULT 74
Q9K802 PRELIMINARY; PRT; 190 AA.
AC Q9K802;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein BH2951.
GN BH2951.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL: AP001517; BAB06670.1; -
DR PIR: G84018; G84018.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 190 AA; 21832 MW; 71F988067DBB21DC CRC64;
Query Match
Best Local Similarity 1.7%; Score 7; DB 16; Length 190;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 165 PLVVANL 171
DB 95 PLVVANL 101
RESULT 75
Q8SW02 PRELIMINARY; PRT; 201 AA.
AC Q8SW02;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein ECU03_1430.
GN ECU03_1430.
OS Encephalitozoon cuniculi.
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.

NCBI_TaxID=6035;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
EX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat P.,
Frensch G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
Encephalitozoon cuniculi."
RL Nature 414:450-453(2001).
CC -1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAS SUBFAMILY.
DR EMBL: AL590443; CAD26286.1; -
DR HSPF: P05713; 3RAB.
DR GO: GO:0005525; F:GTP binding; IEA.
DR GO: GO:0003928; F:RAB small monomeric GTPase activity; IEA.
DR GO: GO:0015031; P:protein transport; IEA.
DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro: IPR003579; GTPase_Rab.
DR InterPro: IPR001806; Ras_trsfmng.
DR InterPro: IPR005225; Small_GTP.
DR Pfam: PF00071; ras; 1.
DR PRINTS: PR00449; RASTRNSFRMNG.
DR SMART: SM00175; RAB; 1.
DR TIGRFAMs: TIGR00231; small_GTP; 1.
KW Hypothetical protein; GTP-Binding; Lipoprotein.
SQ SEQUENCE 201 AA; 22832 MW; 3DE29F8A909619D0 CRC64;
Query Match
Best Local Similarity 1.7%; Score 7; DB 5; Length 201;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 390 TDEIEK 396
DB 132 TDEIEK 138
RESULT 76
O77378 PRELIMINARY; PRT; 202 AA.
AC O77378;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN PFC0795W; MAL386.18.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
EX MEDLINE=9376085; PubMed=1048855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
Gentles S., Gilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
Horrocks P., Jagels K., Jessal B., Kyes S., McLean J., Moule S.,
Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
falciparum."
RL Nature 400:532-538(1999).
DR EMBL: Z98551; CAB1134.1; -
DR PIR: T18495; T18495.
KW Hypothetical protein.
SQ SEQUENCE 202 AA; 24412 MW; 91D8293B96F71CE9 CRC64;

Query Match 1.7%; Score 7; DB 5; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LKKILSN 91
DB 112 LKKILSN 118

RESULT 77
Q9N9M4 PRELIMINARY; PRT; 216 AA.
ID Q9N9M4
AC Q9N9M4
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Probable possible programmed cell death protein, copy 1.
GN L3665.02 OR P265.03.
OS Leishmania major.
OC Eukaryota; Eucelozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5684;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Aert R., Robben J., Weltjens I., Grymonprez B., Volckaert G.,
RA Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Robben J., Grymonprez B., Weltjens I., Aert R., Volckaert G.,
RA Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL359775; CAB95247.1; -;
DR EMBL; AL359716; CAC33967.1; -;
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 4.
DR ProDom; PD000012; EF-hand; 1.
DR SMART; SM00054; EPH; 2.
DR PROSITE; PS00018; EF_HAND; 2.
SQ SEQUENCE 216 AA; 23808 MW; E384F6F1BF9DC278 CRC64;

Query Match 1.7%; Score 7; DB 5; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LSGFVLG 16
DB 146 LSGFVLG 152

RESULT 78
Q9S436 PRELIMINARY; PRT; 220 AA.
ID Q9S436
AC Q9S436
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE M protein precursor (Fragment).
GN EMM.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.

OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SS1551;
RA Beall B.;
RT "New M protein gene sequence type st4264 from Malaysia isolate.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF163684; AAD49332.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M repeat.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF02370; M; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 23 POTENTIAL.
FT CHAIN 24 >220 M PROTEIN.
FT NON_TER 220 220
SQ SEQUENCE 220 AA; 25597 MW; ED900EE15458D2E4 CRC64;

Query Match 1.7%; Score 7; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KREIEKR 257
DB 145 KREIEKR 151

RESULT 79
Q8U0K7 PRELIMINARY; PRT; 221 AA.
ID Q8U0K7
AC Q8U0K7
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein PF1580.
GN PF1580.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010258; AAL81704.1; -;
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR004087; KH_dom.
DR InterPro; IPR003019; KH_prot.
DR Pfam; PF00013; KH; 1.
DR SMART; SM00322; KH; 2.
DR PROSITE; PS00084; KH_TYPE_1; 2.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 221 AA; 25495 MW; 26C00FCBF8E47B9 CRC64;

Query Match 1.7%; Score 7; DB 17; Length 221;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KREIEKR 257
DB 58 KREIEKR 64

RESULT 80
Q8ED42 PRELIMINARY; PRT; 227 AA.
ID Q8ED42
AC Q8ED42
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Acyl-CoA thioesterase I, putative.
GN SO2928.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Altheromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NR-1;
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Meche B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Benan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Ramakrishna S., Weidman J., Imbraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Uterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Nealon K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123 (2002).
RL EMBL; AF015731; JN55942.1; -.
DR TIGR; SO2928; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR InterPro; IPR001087; Lipase_GDSL.
DR Pfam; PF00857; Lipase_GDSL; 1.
KW Complete proteome.
SQ SEQUENCE 227 AA; 25117 MW; 40466A0F8BFB9CA4 CRC64;
Query Match 1.7%; Score 7; DB 16; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 GMSEQLG 178
DB 64 GMSEQLG 70
RESULT 81
ID O01329 PRELIMINARY; PRT; 228 AA.
AC O01329;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE F46A8.3 protein.
GN F46A8.3
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Harris B.R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology";
RL Science 282:2012-2018 (1998).
DR EMBL; Z81539; CAB04389.1; -.
DR PIR; T22259; T22259.
DR WormPep; F46A8.3; CE10562.
DR InterPro; IPR008985; ConA-like lec_gl.
DR InterPro; IPR001079; Galactin.
DR Pfam; PF00337; Gal-bind lectin; 1.
DR SMART; SM00276; GLECT; 1.
SQ SEQUENCE 228 AA; 26022 MW; B82D33036F1EBB0F CRC64;
Query Match 1.7%; Score 7; DB 5; Length 228;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 130 LVFLLLT 136
DB 3 LVFLLLT 9
RESULT 82
QY Q8Y2U4 PRELIMINARY; PRT; 236 AA.
ID Q8Y2U4;
AC Q8Y2U4;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Putative peremease transmembrane protein.
GN RSC0338 OR S00670.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Bottier P., Camus J.C., Catolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaepin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Sigutier P., Thebault P., Whalen M., Wincker F., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502 (2002).
RL EMBL; AL646058; CAD13766.1; -.
KW Complete proteome.
SQ SEQUENCE 236 AA; 24140 MW; 54417628C19BE432 CRC64;
Query Match 1.7%; Score 7; DB 16; Length 236;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 VLGALAF 20
DB 207 VLGALAF 213
RESULT 83
QY Q9K6G9 PRELIMINARY; PRT; 237 AA.
ID Q9K6G9;
AC Q9K6G9; (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE ATP synthase A chain (protein 6).
GN ATPB OR BH3760.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331 (2000).
CC -!- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
CC DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE
CC (BY SIMILARITY).
CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS. CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE

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CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
CC EMBL: AF001519; BAB07479.1; -.
CC FIR; H84119; H84119.
CC DR HSSP; P00855; IC17.
CC DR GO; GO:0015021; C: integral to membrane; IEA.
CC DR GO; GO:0015078; F: hydrolase ion transporter activity; IEA.
CC DR GO; GO:0016787; F: hydrolase activity; IEA.
CC DR GO; GO:0015992; P: proton transport; IEA.
CC DR InterPro; IPR000568; ATPase_Asub.
CC DR Pfam; PF00119; ATP_synt_A; 1.
CC DR PRINTS; PR0123; ATPASEA.
CC DR TIGRFAMs; TIGR01131; ATP_synt_6_or_A; 1.
CC DR PROSITE; PS00449; ATPASE_A; 1.
CC KW CF(0); Hydrolase ion transport; Hydrolase; Transmembrane;
CC Complete proteome.
CC SQ SEQUENCE 237 AA; 26974 MW; 6184C9BB0B401998 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 237;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 MKGFGEY 403
DB 135 MKGFGEY 141

RESULT 84
Q9NJQ3 PRELIMINARY; PRT; 239 AA.
AC Q9NJQ3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Triptophan hydroxylase (Fragment).
OS Lymnaea stagnalis (Great pond snail).
CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
CC Lymnaeidae; Lymnaeidae; Lymnaea.
CC NCBI_TaxID=6523;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21359676; PubMed=11466431;
RA Koert C.E., Spencer G.E., van Minnen J., Li K.W., Geraerts W.P.,
RA Syed N.I., Smit A.B., van Kesteren R.E.;
RA "Functional implications of neurotransmitter expression during axonal
RT regeneration: serotonin, but not peptides, auto-regulate axon growth
RT of an identified central neuron.";
RL J. Neurosci. 21:5597-5606(2001).
DR EMBL; AF129815; AAF36488.1; -.
DR HSSP; P04176; 1PHZ.
DR GO; GO:0005506; F: iron ion binding; IEA.
DR GO; GO:0004497; F: monooxygenase activity; IEA.
DR GO; GO:0009072; P: aromatic amino acid family metabolism; IEA.
DR InterPro; IPR001273; Aaa_hydroxylase.
DR Pfam; PF00351; bioppterin_H; 1.
DR PRINTS; PR00372; FWHYDRXLASE.
DR PRODOM; PD002559; Aaa_hydroxylase; 1.
DR PROSITE; PS00367; BIOPPTERIN_HYDROXYL; 1.
FT NON_TER 1
FT NON_TER 239
FT NON_TER 239
SQ SEQUENCE 239 AA; 28001 MW; D721BD16C7D7B194 CRC64;

Query Match 1.7%; Score 7; DB 5; Length 239;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 VNRKRE 253
DB 29 VNRKRE 35

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RESULT 85
Q816W1 PRELIMINARY; PRT; 242 AA.
AC Q816W1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70).
GN BC4704.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CC NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Golsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017013; AAP11609.1; -.
DR GO; GO:0016829; P: lyase activity; IEA.
DR GO; GO:0004730; F: pseudouridylate synthase activity; IEA.
DR GO; GO:0003723; F: RNA binding; IEA.
DR InterPro; IPR006145; Pseudou_synth.
DR InterPro; IPR000748; Psi_synth_RSU.
DR InterPro; IPR002942; S4.
DR Pfam; PF00849; Pseudou_synth_2; 1.
DR Pfam; PF01479; S4; 1.
DR SMART; SM00363; S4; 1.
DR TIGRFAMs; TIGR00093; TIGR00093; 1.
DR PROSITE; PS01149; PSI_RSU; 1.
DR PROSITE; PS00889; S4; 1.
DR KW Lyase; Complete proteome.
DR SQ SEQUENCE 242 AA; 27503 MW; 6B64557FE60F9CB CRC64;

Query Match 1.7%; Score 7; DB 16; Length 242;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 DTGFFLL 34
DB 105 DTGFFLL 111

RESULT 86
Q8K1L4 PRELIMINARY; PRT; 244 AA.
AC Q8K1L4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to C-type (Calcium dependent, carbohydrate recognition domain)
DE lectin, superfamily member 12.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027742; AAH27742.1; -.
DR GO; GO:0005529; F: sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PS00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

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SQ		SEQUENCE	244 AA; 27542 MW; F50158025FA80C2A CRC64;
Query Match		1.7%; Score 7; DB 11; Length 244;	
Best Local Similarity		100.0%; Pred. No. 2.1e+02;	
Matches		7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	14	VLGALAF 20	
Db	63	VLGALAF 69	
RESULT 87			
Q9J150			
ID	Q9J150	PRELIMINARY;	PRT; 244 AA.
AC	Q9J150;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Dendritic cell-associated C-type lectin-1.		
GN	CLEC5F12 OR DECTN-1.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BALB/c;		
RX	MEDLINE=20347934; PubMed=10779524;		
RA	Arlizumi K., Shen G.-L., Shikano S., Xu S., Ritter R. III,		
RA	Kumamoto T., Edelbaum D., Morita A., Bergstresser P.R., Takashima A.;		
RT	"Identification of a novel, dendritic cell-associated molecule,		
RT	lectin-1, by subtractive cDNA cloning."		
RL	J. Biol. Chem. 275:20157-20167 (2000).		
DR	EMBL; AF262985; AAF72710.1; -.		
DR	MGI; 1861431; Clec5f12.		
DR	GO; GO:0005529; F:sugar binding; IEA.		
DR	GO; GO:0007157; P:heterophilic cell adhesion; IEA.		
DR	InterPro; IPR001304; Lectin_C.		
DR	Fam; PF00059; lectin_c; 1.		
DR	SMART; SM00034; CLECT; 1.		
DR	PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.		
KW	Lectin.		
SQ		SEQUENCE	244 AA; 27621 MW; 55A71C04E68CA002 CRC64;
Query Match		1.7%; Score 7; DB 11; Length 244;	
Best Local Similarity		100.0%; Pred. No. 2.1e+02;	
Matches		7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	14	VLGALAF 20	
Db	63	VLGALAF 69	
RESULT 88			
Q95LW2			
ID	Q95LW2	PRELIMINARY;	PRT; 245 AA.
AC	Q95LW2;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Hypothetical protein.		
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
OC	Cercopithecinae; Macaca.		
OC	NCBI_TaxID=9541;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Testis;		
RA	Hashimoto K., Osada N., Kusuda J., Tanuma R., Hirai M.,		
RA	Terao K., Sugano S.;		
RT	"Isolation of novel full-length cDNA clones from macaque testis cDNA		
RT	libraries."		
SQ		SEQUENCE	245 AA; 27356 MW; D41F6850ADCE7A49 CRC64;
Query Match		1.7%; Score 7; DB 10; Length 245;	
Best Local Similarity		100.0%; Pred. No. 2.1e+02;	
Matches		7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	6	TSVAVLSG 12	
Db	169	TSVAVLSG 175	
RESULT 90			
Q81B21			
ID	Q81B21	PRELIMINARY;	PRT; 247 AA.

RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB071079; BAB64472.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 245 AA; 28822 MW; 2B0B5FC4E969CF03 CRC64;			
Query Match				
Best Local Similarity 1.7%; Score 7; DB 6; Length 245;				
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	31	GFLGGEV 37		
Db	31	GFLGGEV 37		
RESULT 89				
Q9SNW9	PRELIMINARY; PRT; 245 AA.			
ID	Q9SNW9			
AC	Q9SNW9;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Putative transcription factor (Transcription factor-like).			
GN	MYB99			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.			
OC	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RA	Stracke R., Weisshaar B.;			
RT	"R2R3-MYB transcription factor gene nomenclature in Arabidopsis			
RT	thaliana.";			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=COLUMBIA;			
RX	MEDLINE=20181125; PubMed=10718197;			
RA	Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,			
RA	Tabata S.;			
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence			
RT	features of the regions of 3,076,755 bp covered by sixty P1 and TAC			
RT	clones.";			
RL	DNA Res. 7:31-63 (2000).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	-1- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.			
DR	EMBL; AF199026; AAF06022.1; -.			
DR	EMBL; AB019235; BAA97196.1; -.			
DR	HSP; P06876; IMBK.			
DR	GO; GO:0005634; C:nucleus; IEA.			
DR	GO; GO:0003677; F:DNA binding; IEA.			
DR	InterPro; IPR001005; Myb_DNA_binding.			
DR	Pfam; PF00249; myb_DNA-binding; 2.			
DR	SMART; SM00717; SANT; 2.			
DR	PROSITE; PS00037; MYB_1; 1.			
DR	PROSITE; PS00334; MYB_2; 1.			
DR	PROSITE; PS00090; MYB_3; 2.			
KW	DNA-binding; Nuclear protein.			
SQ	SEQUENCE 245 AA; 27356 MW; D41F6850ADCE7A49 CRC64;			
Query Match				
Best Local Similarity 1.7%; Score 7; DB 10; Length 245;				
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	6	TSVAVLSG 12		
Db	169	TSVAVLSG 175		
RESULT 90				
Q81B21	PRELIMINARY; PRT; 247 AA.			
ID	Q81B21			

AC Q81B21;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN MAL81.66.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=3629;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
 RA Quail M., Barrell B.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AL844507; CAD51198.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 247 AA; 28410 MW; ACCSE50E7E220CDA CRC64;
 Query Match 1.7%; Score 7; DB 5; Length 247;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 266 REKNQK 272
 DB 231 REKNQK 237
 RESULT 91
 Q82VV9 PRELIMINARY; PRT; 247 AA.
 AC Q82VV9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Survival protein SurE.
 GN SURE OR NE0950.
 OS Nitrosomonas europaea.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
 OC Nitrosomonadaceae; Nitrosomonas.
 OX NCBI_TaxID=915;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19718 / IPO 14298;
 RX MEDLINE=22586410; PubMed=12700255;
 RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
 RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
 RA Arciero D.M., Holmes N.G., Whittaker M.M., Arp D.J.;
 RT "Complete genome sequence of the ammonia-oxidizing bacterium and
 RT obligate chemolithoautotroph Nitrosomonas europaea."
 RL J. Bacteriol. 185:2759-2773 (2003).
 DR EMBL; BX321859; CAD84861.1; -;
 DR InterPro; IPR002828; SurE.
 DR Pfam; PF01975; SurE; 1.
 DR ProDom; PD005378; SurE; 1.
 DR TIGRFAMs; TIGR00087; surE; 1.
 KW Complete proteome.
 SQ SEQUENCE 247 AA; 26851 MW; 173C0E7104B384D1 CRC64;
 Query Match 1.7%; Score 7; DB 16; Length 247;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 29 TEGFLG 35
 DB 110 TEGFLG 116
 RESULT 92
 Q97J11 PRELIMINARY; PRT; 254 AA.
 ID Q97J11
 AC Q97J11;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DS Proline/glycine betaine ABC transport system, ATPase
 DE component.
 GN CAC1475.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum."
 RL J. Bacteriol. 183:4823-4838 (2001).
 DR EMBL; AE007658; AAK79443.1; -;
 DR PIR; H97081; H97081.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 254 AA; 28845 MW; 5172AE884EEAD3BA CRC64;
 Query Match 1.7%; Score 7; DB 16; Length 254;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 251 KREIEK 257
 DB 111 KREIEK 117
 RESULT 93
 Q97Q44 PRELIMINARY; PRT; 257 AA.
 ID Q97Q44
 AC Q97Q44;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Spermidine/putrescine ABC transporter, permease protein.
 GN SPI387.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC BAA-334 / TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae."
 RL Science 293:498-506 (2001).

DR EMBL; AE007436; AAK75485.1; -.
 DR PIR; D95161; D95161.
 DR TIGR; SPI387; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000515; BPD_transp.
 DR Pfam; PF00528; BPD_transp; 1.
 KW Complete proteome.
 SQ SEQUENCE 257 AA; 28978 MW; 4619D7D6328E8C4C CRC64;
 Query Match 1.7%; Score 7; DB 16; Length 257;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 135 LTPSIIT 141
 Db 179 LTPSIIT 185
 RESULT 94
 ID Q9ALL2 PRELIMINARY; PRT; 258 AA.
 AC Q9ALL2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CS12 fimbria upstream putative regulatory protein.
 GN YAHF.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 ON NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=350CI;
 RA Steinland H., Gastra W., Valvatne H., Sommerfelt H.;
 RT "The organization of the enterotoxigenic Escherichia coli CS12 gene cluster is identical to that of the 987P gene cluster";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL REGULATORS.
 CC EMBL; AY009096; AK09065.1; -.
 DR GO; GO:0005222; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR000005; HTHARAC.
 DR Pfam; PF00165; HTH_ARAC; 2.
 DR PRINTS; PR00032; HTHARAC.
 DR SMART; SM00342; HTH_ARAC; 1.
 DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
 DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
 KW DNA-binding; Transcription; Transcription regulation.
 SQ SEQUENCE 258 AA; 25616 MW; 35776C84B93CFE8B CRC64;
 Query Match 1.7%; Score 7; DB 2; Length 258;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 84 ALKKILS 90
 Db 73 ALKKILS 79
 RESULT 95
 ID Q7WZ08 PRELIMINARY; PRT; 264 AA.
 AC Q7WZ08;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE S-adenosylmethionine decarboxylase.

GN SPED.
 OS Lysobacter enzymogenes.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Lysobacter.
 ON NCBI_TaxID=69;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3;
 RA Kobayashi D.Y., Reedy R.M., Palumbo J.D., Yuen G.Y.;
 RT "Transposon insertion within a catabolite activator protein-like protein (cip) gene homolog results in loss of lytic enzyme, antifungal RT and biological control activities expressed by Lysobacter enzymogenes strain C3";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY316743; AAP8140.1; -.
 SQ SEQUENCE 264 AA; 30594 MW; 5D28C7061A412C53 CRC64;
 Query Match 1.7%; Score 7; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 249 RLKREIE 255
 Db 248 RLKREIE 254
 RESULT 96
 ID Q97QX9 PRELIMINARY; PRT; 266 AA.
 AC Q97QX9;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE AEC-2 transporter, permease protein, putative.
 GN SPI063.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 ON NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC BAA-334 / TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtaple E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae";
 RL Science 293:498-506(2001).
 DR EMBL; AE007408; AAK75177.1; -.
 DR PIR; H95122; H95122.
 DR TIGR; SPI063; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti...; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000412; ABC_transp2.
 DR PRINTS; PR00164; ABC2TRANSPORT.
 KW Complete proteome.
 SQ SEQUENCE 266 AA; 30501 MW; F3AA416DC89F4893 CRC64;
 Query Match 1.7%; Score 7; DB 16; Length 266;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 LVFLILT 136
 Db 238 LVFLILT 244

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RESULT 97
Q8ZJC0
ID Q8ZJC0 PRELIMINARY; PRT; 266 AA.
AC Q8ZJC0;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8).
GN FKPA OR YP00135.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA ParKhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebathia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AJ414141; CAC89056.1; -.
DR PIR; AF0024; AF0024.
DR GO; GO:0043027; F:cyclophilin-type peptidyl-prolyl cis-trans . . . ; IEA.
DR GO; GO:0004600; F:cyclophilin; IEA.
DR GO; GO:0030053; F:FK506-sensitive peptidyl-prolyl cis-trans i . . . ; IEA.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR001179; FKBP_Nterm.
DR Pfam; PF00254; FKBP; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR PROSITE; PS00559; FKBP_PPIASE_3; 1.
KW Isomerase; Complete proteome.
SQ SEQUENCE 266 AA; 28573 MW; 1BA343594FFEB4F CRC64;

Query Match 1.7%; Score 7; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEK 396
Db 91 TDEIEK 97

RESULT 98
Q9LH18
ID Q9LH18 PRELIMINARY; PRT; 269 AA.
AC Q9LH18;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Hypothetical protein.
GN F28J15.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

[2]
RN SEQUENCE FROM N.A.
RP STRAIN=COLUMBIA;
RX PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=cv Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansong W., Unseld M.,
RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA DeSerny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA Del Simone V., Choien N., Attiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rued S., Zaccaria P., Mewes H.-W.,
RA Mayer K.P.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Miltischer J., Sellers P., Gill J.E., Feldhlyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822(2000).
DR EMBL; AP002047; BAB03127.1; -.
DR DR EMBL; AP002063; BAB03127.1; JOINED.
DR DR EMBL; AC069472; AAG51075.1; -.
KW Hypothetical protein.
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DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN V13029.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
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RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;

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Job time : 68 secs

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RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.B.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016807; A011353.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 270 AA; 31639 MW; 56D7E1C98598156B CRC64;

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DB 217 EMYASLQ 223
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DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter ATP-binding protein.
GN YLMA OR XCC0161.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
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RX MEDLINE=22022145; PubMed=12024117;
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RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White P.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AF012112; AM39480.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti...; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC tran; 1.
DR PRODOM; PD000006; ABC transporter; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 16, 2004, 10:17:36 ; Search time 23 Seconds
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Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 500 summaries

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- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	7	1.7	111	4	US-09-328-352-5992
4	7	1.7	117	4	US-09-621-976-4623
5	7	1.7	126	4	US-09-453-195A-4
6	7	1.7	137	3	US-09-446-504-34
7	7	1.7	137	4	US-09-712-266-34
8	7	1.7	182	4	US-09-540-236-2904
9	7	1.7	244	3	US-08-772-440-2
10	7	1.7	257	1	US-07-956-700B-105
11	7	1.7	257	1	US-08-476-537-105
12	7	1.7	257	1	US-08-485-607-105
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22	7	1.7	296	4	US-08-455-973-11
23	7	1.7	319	4	US-09-910-174B-12
24	7	1.7	319	4	US-09-620-461-12
25	7	1.7	321	3	US-08-748-506-13
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139	6	1.5	147	4	US-09-328-352-7654	Sequence 7654, Ap	212	6	1.5	195	4	US-08-463-682-5	Sequence 5, Appli
140	6	1.5	147	4	US-09-107-532A-7081	Sequence 7081, Ap	213	6	1.5	195	4	US-09-489-039A-11549	Sequence 11549, A
141	6	1.5	149	4	US-09-134-001C-3012	Sequence 3012, Ap	214	6	1.5	195	4	US-09-149-476-353	Sequence 353, App
142	6	1.5	149	4	US-09-328-352-4810	Sequence 4810, Ap	215	6	1.5	195	4	US-08-328-352-7410	Sequence 7410, Ap
143	6	1.5	150	3	US-08-082-877-2	Sequence 2, Appli	216	6	1.5	195	4	US-09-252-991A-30119	Sequence 30119, A
144	6	1.5	150	4	US-09-709-790-2	Sequence 2, Appli	217	6	1.5	195	4	US-08-797-689-4	Sequence 4, Appli
145	6	1.5	151	4	US-08-134-000C-5616	Sequence 5616, Ap	218	6	1.5	195	4	US-09-252-991A-32109	Sequence 32109, Ap
146	6	1.5	156	4	US-09-252-991A-20612	Sequence 20612, A	219	6	1.5	195	4	US-09-134-000C-5239	Sequence 5239, Ap
147	6	1.5	158	4	US-09-252-991A-18463	Sequence 18463, A	220	6	1.5	195	4	US-09-205-258-385	Sequence 385, App
148	6	1.5	158	4	US-09-808-701A-20	Sequence 85, Appl	221	6	1.5	195	4	US-09-252-991A-31286	Sequence 31286, A
149	6	1.5	159	4	US-08-311-731A-85	Sequence 85, Appl	222	6	1.5	195	4	US-09-634-238-353	Sequence 353, App
150	6	1.5	160	2	US-08-602-941-1	Sequence 1, Appli	223	6	1.5	195	4	US-09-396-840-3	Sequence 3, Appli
151	6	1.5	160	3	US-08-961-264-1	Sequence 1, Appli	224	6	1.5	195	4	US-09-396-840-3	Sequence 3, Appli
152	6	1.5	160	4	US-08-432-098A-1	Sequence 1, Appli	225	6	1.5	195	4	US-08-961-083-30	Sequence 30, Appl
153	6	1.5	160	4	US-08-612-342-1	Sequence 1, Appli	226	6	1.5	195	4	US-09-252-991A-32484	Sequence 32484, A
154	6	1.5	160	4	US-08-612-421A-1	Sequence 1, Appli	227	6	1.5	195	4	US-09-536-784-30	Sequence 30, Appl
155	6	1.5	160	4	US-09-724-401-1	Sequence 388, App	228	6	1.5	195	4	US-09-543-681A-6305	Sequence 6305, Ap
156	6	1.5	161	4	US-09-615-192A-388	Sequence 388, App	229	6	1.5	195	4	US-09-543-681A-4276	Sequence 4276, Ap
157	6	1.5	163	4	US-09-134-000C-3710	Sequence 3710, Ap	230	6	1.5	195	4	US-08-446-919A-2	Sequence 2, Appli
158	6	1.5	171	4	US-09-198-452A-1184	Sequence 1184, Ap	231	6	1.5	195	4	US-08-611-880-2	Sequence 2, Appli
159	6	1.5	174	4	US-09-149-476-526	Sequence 526, App	232	6	1.5	195	4	US-08-904-284-7	Sequence 7, Appli
160	6	1.5	180	4	US-09-544-716-19	Sequence 19, Appl	233	6	1.5	195	4	US-09-540-236-2730	Sequence 2730, Ap
161	6	1.5	180	4	US-09-557-921-20	Sequence 20, Appl	234	6	1.5	195	4	US-09-252-991A-19583	Sequence 19583, A
162	6	1.5	180	4	US-09-619-380-21	Sequence 21, Appl	235	6	1.5	195	4	US-08-540-236-2404	Sequence 2404, Ap
163	6	1.5	184	4	US-09-134-001C-4555	Sequence 4555, Ap	236	6	1.5	195	4	US-09-155-185-2	Sequence 2, Appli
164	6	1.5	184	4	US-09-134-000C-3779	Sequence 3779, Ap	237	6	1.5	195	4	US-09-338-432A-129	Sequence 129, App
165	6	1.5	185	1	US-07-988-473-2	Sequence 2, Appli	238	6	1.5	195	4	US-09-733-883-4	Sequence 4, Appli
166	6	1.5	185	3	US-08-848-810-25	Sequence 25, Appl	239	6	1.5	195	4	US-08-522-813-4	Sequence 4, Appli
167	6	1.5	185	3	US-09-164-193-21	Sequence 21, Appl	240	6	1.5	195	4	US-09-252-991A-21844	Sequence 21844, A
168	6	1.5	185	4	US-09-221-448A-21	Sequence 21, Appl	241	6	1.5	195	4	US-09-328-352-5958	Sequence 5958, Ap
169	6	1.5	185	5	PCT-US93-12019-2	Sequence 2, Appli	242	6	1.5	195	4	US-09-252-991A-16878	Sequence 16878, A
170	6	1.5	186	4	US-09-198-452A-915	Sequence 915, App	243	6	1.5	195	4	US-09-134-001C-3155	Sequence 3155, Ap
171	6	1.5	187	3	US-08-463-682-1	Sequence 1, Appli	244	6	1.5	195	4	US-09-489-039A-11576	Sequence 11576, A
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252	6	1.5	286	4	US-09-072-596-82	Sequence 82, Appl	325	6	1.5	348	2	US-08-484-397A-3	Sequence 3, Appli
253	6	1.5	286	4	US-09-252-991A-27746	Sequence 27746, A	326	6	1.5	348	2	US-08-484-397A-4	Sequence 4, Appli
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257	6	1.5	290	4	US-09-543-681A-6454	Sequence 6454, Ap	330	6	1.5	348	2	US-08-484-397A-27	Sequence 27, Appl
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260	6	1.5	293	2	US-08-896-885-5	Sequence 5, Appli	333	6	1.5	351	3	US-08-466-465-6	Sequence 6, Appli
261	6	1.5	293	4	US-09-375-256-5	Sequence 5, Appli	334	6	1.5	353	3	US-09-461-474-4	Sequence 4, Appli
262	6	1.5	293	4	US-09-561-756-21	Sequence 21, Appl	335	6	1.5	353	4	US-09-252-991A-13098	Sequence 3098, A
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266	6	1.5	293	4	US-08-724-378D-6	Sequence 6, Appli	339	6	1.5	359	1	US-08-120-827-2	Sequence 2, Appli
267	6	1.5	293	4	US-09-516-747-31	Sequence 31, Appl	340	6	1.5	359	1	US-08-478-675-2	Sequence 2, Appli
268	6	1.5	293	4	US-09-954-697-21	Sequence 21, Appl	341	6	1.5	361	4	US-09-328-352-5459	Sequence 5459, Ap
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273	6	1.5	295	4	US-09-328-352-5192	Sequence 5192, Ap	346	6	1.5	373	3	US-09-039-198A-14	Sequence 14, Appl
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275	6	1.5	296	4	US-09-489-039A-14102	Sequence 14102, A	348	6	1.5	373	4	US-08-877-599-14	Sequence 14, Appl
276	6	1.5	296	3	US-09-080-044-9	Sequence 9, Appli	349	6	1.5	373	4	US-08-877-599-15	Sequence 15, Appl
277	6	1.5	298	4	US-09-531-857A-9	Sequence 9, Appli	350	6	1.5	373	4	US-09-267-574-14	Sequence 14, Appl
278	6	1.5	298	4	US-09-543-681A-6110	Sequence 6110, Ap	351	6	1.5	373	4	US-09-267-574-15	Sequence 15, Appl
279	6	1.5	301	4	US-09-328-352-6885	Sequence 6885, Ap	352	6	1.5	375	1	US-08-205-719-2	Sequence 2, Appli
280	6	1.5	302	4	US-08-957-351-3	Sequence 3, Appli	353	6	1.5	375	3	US-08-746-883-5	Sequence 5, Appli
281	6	1.5	302	4	US-08-957-351-7	Sequence 7, Appli	354	6	1.5	375	4	US-09-573-906-2	Sequence 2, Appli
282	6	1.5	302	4	US-08-957-351-30	Sequence 30, Appl	355	6	1.5	375	4	US-09-252-991A-27411	Sequence 27411, A
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284	6	1.5	304	4	US-09-609-816-5	Sequence 5, Appli	357	6	1.5	376	2	US-08-709-923-4	Sequence 4, Appli
285	6	1.5	304	4	US-09-107-532A-7041	Sequence 7041, Ap	358	6	1.5	378	4	US-09-789-300A-4	Sequence 4, Appli
286	6	1.5	304	4	US-09-489-039A-11956	Sequence 11956, A	359	6	1.5	380	3	US-08-857-076-110	Sequence 110, App
287	6	1.5	305	4	US-09-107-532A-5486	Sequence 5486, Ap	360	6	1.5	382	4	US-09-057-996-17	Sequence 17, Appl
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290	6	1.5	309	4	US-09-134-001C-3039	Sequence 3039, Ap	363	6	1.5	386	4	US-09-328-352-7130	Sequence 7130, Ap
291	6	1.5	311	3	US-08-961-083-184	Sequence 184, App	364	6	1.5	387	2	US-08-486-839-6	Sequence 6, Appli
292	6	1.5	311	4	US-09-328-352-6665	Sequence 6665, Ap	365	6	1.5	387	3	US-09-151-011-6	Sequence 6, Appli
293	6	1.5	311	4	US-09-536-784-184	Sequence 184, App	366	6	1.5	387	4	US-09-343-623-6	Sequence 6, Appli
294	6	1.5	312	4	US-09-252-991A-31853	Sequence 31853, A	367	6	1.5	388	4	US-09-880-137-5	Sequence 5, Appli
295	6	1.5	312	4	US-08-957-351-9	Sequence 9, Appli	368	6	1.5	388	4	US-09-880-137-5	Sequence 6, Appli
296	6	1.5	313	4	US-09-198-452A-205	Sequence 205, App	369	6	1.5	389	4	US-09-788-657-23	Patent No. 5240849
297	6	1.5	313	4	US-09-134-000C-6101	Sequence 6101, Ap	370	6	1.5	389	4	US-09-679-279-5	Sequence 5, Appli
298	6	1.5	314	4	US-09-252-991A-27537	Sequence 27537, A	371	6	1.5	390	4	US-09-107-532A-6425	Sequence 6425, Ap
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308	6	1.5	324	4	US-09-134-001C-5525	Sequence 5525, Ap	381	6	1.5	401	2	US-08-839-008-5	Sequence 5, Appli
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311	6	1.5	331	4	US-09-252-991A-24420	Sequence 24420, A	384	6	1.5	410	4	US-09-252-991A-19675	Sequence 19675, A
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313	6	1.5	333	3	US-08-960-780-44	Sequence 44, Appl	386	6	1.5	414	1	US-09-337-913-1	Sequence 1, Appli
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316	6	1.5	334	2	US-08-484-397A-8	Sequence 8, Appli	389	6	1.5	419	2	US-08-270-581-2	Sequence 2, Appli
317	6	1.5	334	2	US-08-665-647-3	Sequence 3, Appli	390	6	1.5	419	4	US-09-146-893-2	Sequence 5, Appli
318	6	1.5	336	4	US-09-107-532A-6417	Sequence 6417, Ap	391	6	1.5	419	4	US-08-675-499A-5	
319	6	1.5	340	4	US-09-543-681A-7850	Sequence 7850, Ap	392	6	1.5	419	4		

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396	6	1.5	420	4	US-09-168-595-142	Sequence 142, App
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404	6	1.5	425	3	US-09-274-570-3	Sequence 3, Appli
405	6	1.5	425	4	US-09-489-039A-9445	Sequence 9445, Ap
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411	6	1.5	437	4	US-08-540-236-2207	Sequence 2207, Ap
412	6	1.5	439	3	US-09-413-814-13	Sequence 13, Appl
413	6	1.5	439	4	US-09-129-668-6	Sequence 6, Appli
414	6	1.5	441	4	US-09-254-776B-79	Sequence 79, Appl
415	6	1.5	441	4	US-09-543-681A-7207	Sequence 7207, Ap
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418	6	1.5	444	4	US-09-352-991A-31066	Sequence 31066, A
419	6	1.5	446	2	US-08-574-138-6	Sequence 6, Appli
420	6	1.5	446	3	US-08-879-941-2	Sequence 2, Appli
421	6	1.5	446	3	US-09-457-046B-74	Sequence 74, Appl
422	6	1.5	446	4	US-09-747-116-2	Sequence 2, Appli
423	6	1.5	446	4	US-09-761-716-2	Sequence 2, Appli
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426	6	1.5	454	3	US-06-793-624-33	Sequence 33, Appl
427	6	1.5	454	5	PCT-US95-10194-33	Sequence 33, Appl
428	6	1.5	459	4	US-09-489-039A-9027	Sequence 9027, Ap
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441	6	1.5	466	4	US-09-267-574-4	Sequence 4, Appli
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443	6	1.5	468	3	US-09-022-523-8	Sequence 8, Appli
444	6	1.5	468	3	US-09-802-633-8	Sequence 8, Appli
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447	6	1.5	472	4	US-09-504-357-2	Sequence 2, Appli
448	6	1.5	474	3	US-09-022-699-2	Sequence 2, Appli
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452	6	1.5	475	1	US-08-587-389-2	Sequence 2, Appli
453	6	1.5	477	4	US-09-252-991A-22197	Sequence 22197, A
454	6	1.5	480	3	US-09-171-482-2	Sequence 2, Appli
455	6	1.5	482	4	US-09-107-532A-5672	Sequence 5672, Ap
456	6	1.5	483	4	US-09-252-991A-27160	Sequence 27160, A
457	6	1.5	483	4	US-09-252-991A-29267	Sequence 29267, A
458	6	1.5	488	1	US-08-190-802A-60	Sequence 60, Appl
459	6	1.5	488	3	US-08-477-346-60	Sequence 60, Appl
460	6	1.5	488	4	US-08-473-089-60	Sequence 60, Appl
461	6	1.5	488	4	US-08-487-072A-60	Sequence 60, Appl
462	6	1.5	493	4	US-09-252-991A-26260	Sequence 26260, A
463	6	1.5	493	4	US-09-252-991A-31526	Sequence 31526, A
464	6	1.5	494	1	US-08-014-723-14	Sequence 14, Appl
465	6	1.5	494	1	US-08-014-723-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-621-976-3917
; Sequence 3917, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3917
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19..-1
US-09-621-976-3917

Query March 36.9%; Score 151; DB 4; Length 151;

Best Local Similarity 100.0%; Pred.No. 5.6e-144;

Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEESTSAVLSGFLVGCALAFQHLNLTSDTEGFLIGVKGEAKNSITDSQMDVWVYITD 60

Db 1 MGEESTSAVLSGFLVGCALAFQHLNLTSDTEGFLIGVKGEAKNSITDSQMDVWVYITD 60

QY 61 IOKYPCYOLFVFNSSGEVNEQALKILSNVKNVGVYFRHRSQIMTFRERLHKN 120

Db 61 IQKVPQVQLSFYNSGEVNEQALKILSNVKNVGVYKFRHRSDQIMFRERLLHKN 120
QY 121 LQEHFSNODLVFLLLTPSIITSCSTHRLH 151
Db 121 LQEHFSNODLVFLLLTPSIITSCSTHRLH 151

RESULT 2
US-09-543-681A-6080
; Sequence 6080, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6080
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6080

Query Match 1.7%; Score 7; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 LTPSIIT 141
Db 30 LTPSIIT 36

RESULT 3
US-09-328-352-5992
; Sequence 5992, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5992
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5992

Query Match 1.7%; Score 7; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 LTPSIIT 141
Db 34 LTPSIIT 40

RESULT 4
US-09-621-976-4623
; Sequence 4623, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTE and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2

Db 61 IQKVPQVQLSFYNSGEVNEQALKILSNVKNVGVYKFRHRSDQIMFRERLLHKN 120
QY 121 LQEHFSNODLVFLLLTPSIITSCSTHRLH 151
Db 121 LQEHFSNODLVFLLLTPSIITSCSTHRLH 151

RESULT 5
US-09-453-195A-4
; Sequence 4, Application US/09453195A
; Patent No. 6368826
; GENERAL INFORMATION:
; APPLICANT: Ligensa, Tanja
; APPLICANT: Schumacher, Ralf
; TITLE OF INVENTION: IGF-1 Receptor Interacting Proteins
; FILE REFERENCE: 09/453,195
; CURRENT APPLICATION NUMBER: US/09/453,195A
; CURRENT FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: EPO 98122992.5
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Xaa at position 123 is any one of the twenty naturally occurring
US-09-453-195A-4

Query Match 1.7%; Score 7; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 SSPETDE 392
Db 61 SSPETDE 67

RESULT 6
US-09-446-504-34
; Sequence 34, Application US/09446504
; Patent No. 6218150
; GENERAL INFORMATION:
; APPLICANT: UEMORI, Takashi
; APPLICANT: SATO, Yoshimi
; APPLICANT: FUJITA, Tomoko
; APPLICANT: MIYAKE, Kazuo
; APPLICANT: MUKAI, Hiroyuki

Db 61 SSPETDE 67

; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4623
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 35
; OTHER INFORMATION: Xaa = *,Tip
; NAME/KEY: UNSURE
; LOCATION: 48
; OTHER INFORMATION: Xaa = Ala,Pro
; NAME/KEY: UNSURE
; LOCATION: 36
; OTHER INFORMATION: Xaa = Asp,His
US-09-621-976-4623

Query Match 1.7%; Score 7; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 ERLHKN 120
Db 19 ERLHKN 25

RESULT 5
US-09-453-195A-4
; Sequence 4, Application US/09453195A
; Patent No. 6368826
; GENERAL INFORMATION:
; APPLICANT: Ligensa, Tanja
; APPLICANT: Schumacher, Ralf
; TITLE OF INVENTION: IGF-1 Receptor Interacting Proteins
; FILE REFERENCE: 09/453,195
; CURRENT APPLICATION NUMBER: US/09/453,195A
; CURRENT FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: EPO 98122992.5
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Xaa at position 123 is any one of the twenty naturally occurring
US-09-453-195A-4

Query Match 1.7%; Score 7; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 SSPETDE 392
Db 61 SSPETDE 67

RESULT 6
US-09-446-504-34
; Sequence 34, Application US/09446504
; Patent No. 6218150
; GENERAL INFORMATION:
; APPLICANT: UEMORI, Takashi
; APPLICANT: SATO, Yoshimi
; APPLICANT: FUJITA, Tomoko
; APPLICANT: MIYAKE, Kazuo
; APPLICANT: MUKAI, Hiroyuki

Db 61 SSPETDE 67

; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
; FILE REFERENCE: 1422-408PCT
; CURRENT APPLICATION NUMBER: US/09/446,504
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/JP98/02845
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: JP 9-187496
; PRIOR FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: JP 9-320692
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Pyrococcus furiosus
US-09-446-504-34

Query Match 1.7%; Score 7; DB 3; Length 137;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 EEIEKMK 398
Db 98 EEIEKMK 104
|||||

RESULT 7
US-09-712-266-34
; Sequence 34, Application US/09712266
; Patent No. 6333158
; GENERAL INFORMATION:
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
; FILE REFERENCE: 1422-408PCT
; CURRENT APPLICATION NUMBER: US/09/712,266
; CURRENT FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 09/446,504
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/JP98/02845
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: JP 9-187496
; PRIOR FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: JP 9-320692
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Pyrococcus furiosus
US-09-712-266-34

Query Match 1.7%; Score 7; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 EEIEKMK 398
Db 98 EEIEKMK 104
|||||

RESULT 8
US-09-540-236-2904
; Sequence 2904, Application US/09540236

; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2904
; LENGTH: 182
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-2904

Query Match 1.7%; Score 7; DB 4; Length 182;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LKXILSN 91
Db 174 LKXILSN 180
|||||

RESULT 9
US-08-772-440-2
; Sequence 2, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Arizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-2

Query Match 1.7%; Score 7; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VLGLALP 20
Db 63 VLGLALP 69
|||||

```
RESULT 10
US-07-956-700B-105
; Sequence 105, Application US/07956700B
; Patent No. 5539092
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,700B
; FILING DATE: 19921002
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5539092thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-07-956-700B-105

Query Match 1.7%; Score 7; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 389 ETDEEIE 395
Db 112 ETDEEIE 118

RESULT 11
US-08-476-537-105
; Sequence 105, Application US/08476537
; Patent No. 5756290
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5756290th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-476-537-105
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US-07-956-700B-105
; Sequence 105, Application US/07956700B
; Patent No. 5539092
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,700B
; FILING DATE: 19921002
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5539092thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-476-537-105

Query Match 1.7%; Score 7; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 389 ETDEEIE 395
Db 112 ETDEEIE 118

RESULT 12
US-08-485-607-105
; Sequence 105, Application US/08485607
; Patent No. 5792627
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-485-607-105
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; MOLECULE TYPE: Peptide
US-08-485-607-105

Query Match      1.7%; Score 7; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      389 ETDEIE 395
Db      112 ETDEIE 118

RESULT 13
US-08-475-879-105
; Sequence 105, Application US/08475879
; Patent No. 5972644
; Patent No. 5972644 5786170
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,879
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5972644 5786170thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-475-879-105

Query Match      1.7%; Score 7; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      389 ETDEIE 395
Db      112 ETDEIE 118

RESULT 14
US-09-433-043B-105
; Sequence 105, Application US/09433043B
; Patent No. 6393342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR

; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 105
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-433-043B-105

Query Match      1.7%; Score 7; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      389 ETDEIE 395
Db      112 ETDEIE 118

RESULT 15
US-07-941-523-23
; Sequence 23, Application US/07941523
; Patent No. 5571718
; GENERAL INFORMATION:
; APPLICANT: Dunn, John J
; APPLICANT: Barbour, Alan G
; TITLE OF INVENTION: Cloning and Expression of Borrelia
; TITLE OF INVENTION: Lipoproteins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 01730
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/941,523
; FILING DATE: 19920908
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: BNL90-01A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-941-523-23

Query Match      1.7%; Score 7; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 250 LKREIEK 256
Db 197 LKREIEK 203

RESULT 16
US-09-540-236-2036
; Sequence 2036, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709,2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2036
; LENGTH: 286
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2036

Query Match 1.7%; Score 7; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 ASTPQII 344
Db 194 ASTPQII 200

RESULT 17
US-08-320-161-11
; Sequence 11, Application US/08320161
; Patent No. 5747294
; GENERAL INFORMATION:
; APPLICANT: Flavell, Richard A.
; APPLICANT: Kantor, Fred S.
; APPLICANT: Barthold, Stephen W.
; APPLICANT: Fikrig, Erol
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE PREVENTION AND DIAGNOSIS OF LYME DISEASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022-6250
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,161
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/682,355
; FILING DATE:
; APPLICATION NUMBER: US 538,969
; FILING DATE: 15-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 602,551
; FILING DATE: 26-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: YU-100 CIP 2

QY 250 LKREIEK 256
Db 212 LKREIEK 218

RESULT 18
US-08-137-175A-3
; Sequence 3, Application US/08137175A
; Patent No. 5777095
; GENERAL INFORMATION:
; APPLICANT: BARBOUR, Alan G.
; APPLICANT: BERGSTROM, Sven
; APPLICANT: HANSSON, Lennart
; TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND
; TITLE OF INVENTION: PROPHYLAXIS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,175A
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08972
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: BARBOUR-1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-175A-3

Query Match 1.7%; Score 7; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
Db 212 LKREIEK 218

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 715-0600
; TELEFAX: (212) 715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-320-161-11

Db 212 LKREIEK 218

RESULT 19

US-08-479-017-3

Sequence 3, Application US/08479017

Patent No. 6143872

GENERAL INFORMATION:

APPLICANT: BARBOUR, Alan G.

APPLICANT: BERGSTROM, Sven

APPLICANT: HANSSON, Lennart

TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND

TITLE OF INVENTION: PROPHYLAXIS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/479,017

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/137,175

FILING DATE: 26-OCT-1993

APPLICATION NUMBER: PCT/US92/08972

FILING DATE: 22-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, Iver P.

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: BARBOUR-1B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 296 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-479-017-3

Query Match 1.7%; Score 7; DB 3; Length 296;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256

Db 212 LKREIEK 218

RESULT 20

US-08-455-829-11

Sequence 11, Application US/08455829

Patent No. 6197301

GENERAL INFORMATION:

APPLICANT: Flavell, Richard A.

APPLICANT: Kantor, Fred S.

APPLICANT: Barthold, Stephen W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: PREVENTION AND DIAGNOSIS OF LYME DISEASE

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 875 Third Avenue

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022-6250

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,829

FILING DATE: 31-MAY-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/682,355

FILING DATE: 08-APR-1991

APPLICATION NUMBER: US 538,969

FILING DATE: 15-JUN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 602,551

FILING DATE: 26-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: YU-100 CIP 2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 715-0600

TELEFAX: (212) 715-0673

TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 296 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-455-829-11

Query Match 1.7%; Score 7; DB 3; Length 296;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256

Db 212 LKREIEK 218

RESULT 21

US-08-235-836C-22

Sequence 22, Application US/08235836C

Patent No. 6248562

GENERAL INFORMATION:

APPLICANT: Dunn, John J.

APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising

TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor

NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brookhaven National Laboratory

STREET:

CITY: Upton

STATE: NY

COUNTRY: USA

ZIP: 11973

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/235,836C

FILING DATE: 29-APR-1994

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELEPHONE: (516) 282-7338
TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-235-836C-22

Query Match 1.7%; Score 7; DB 3; Length 296;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
DB 212 LKREIEK 218

RESULT 22
US-08-455-973-11
Sequence 11, Application US/08455973
Patent No. 6344552
GENERAL INFORMATION:
APPLICANT: Flavell, Richard A.
Kantor, Fred S.
Barthold, Stephen W.
Fikrig, Erol
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE PREVENTION AND DIAGNOSIS OF LYME DISEASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 875 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,973
FILING DATE: 31-May-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/320,161
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
APPLICATION NUMBER: US/07/682,355
FILING DATE: <Unknown>
APPLICATION NUMBER: US 538,969
FILING DATE: 15-JUN-1990
APPLICATION NUMBER: US 602,551
FILING DATE: 26-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: YU-100 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 715-0600

US-08-235-836C-22

TELEFAX: (212) 715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-455-973-11

Query Match 1.7%; Score 7; DB 4; Length 296;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
DB 212 LKREIEK 218

RESULT 23
US-09-910-174B-12
Sequence 12, Application US/09910174B
Patent No. 6630575
GENERAL INFORMATION:
APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
TITLE OF INVENTION: Family and Uses Thereof
FILE REFERENCE: 35800/236924
CURRENT APPLICATION NUMBER: US/09/910,174B
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/620,461
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-09-910-174B-12

Query Match 1.7%; Score 7; DB 4; Length 319;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SQOEELK 227
DB 307 SQOEELK 313

RESULT 24
US-09-620-461-12
Sequence 12, Application US/09620461
Patent No. 6635750
GENERAL INFORMATION:
APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
TITLE OF INVENTION: Family and Uses Thereof
FILE REFERENCE: 5800-149
CURRENT APPLICATION NUMBER: US/09/620,461
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-09-620-461-12

Query Match 1.7%; Score 7; DB 4; Length 319;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SLOEELK 227
DB 307 SLOEELK 313

RESULT 25
US-08-748-506-13
Sequence 13, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Rohnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-748-506-13

Query Match 1.7%; Score 7; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 ALKKILS 90
DB 312 ALKKILS 318

RESULT 26
US-08-724-394A-6
Sequence 6, Application US/08724394A
Patent No. 587237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Pitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1.342
OTHER INFORMATION: /note= "BTF4"

US-08-724-394A-6

Query Match 1.7%; Score 7; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SLOEELK 227
DB 330 SLOEELK 336

RESULT 27
US-09-910-174B-14
Sequence 14, Application US/09910174B
Patent No. 6630575
GENERAL INFORMATION:
APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
FILE REFERENCE: 35800/236924
CURRENT APPLICATION NUMBER: US/09/910,174B
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/620,461
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-09-910-174B-14

Query Match 1.7%; Score 7; DB 4; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 221 SLQEELK 227
    |||||
Db 305 SLQEELK 311

RESULT 28
US-09-620-461-14
; Sequence 14, Application US/09620461
; Patent No. 6635750
; GENERAL INFORMATION:
; APPLICANT: Coyne, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
; FILE REFERENCE: 5800-149
; CURRENT APPLICATION NUMBER: US/09/620,461
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-461-14

Query Match 1.7%; Score 7; DB 4; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SLQEELK 227
    |||||
Db 305 SLQEELK 311

RESULT 29
US-08-235-836C-118
; Sequence 118, Application US/08235836C
; Patent No. 6248562
; GENERAL INFORMATION:
; APPLICANT: Dunn, John J.
; APPLICANT: Luft, Benjamin J.
; TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
; TITLE OF INVENTION: Borrelia Polyptides and Uses Therefor
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brookhaven National Laboratory
; STREET:
; CITY: Upton
; STATE: NY
; COUNTRY: USA
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,836C
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,191
; FILING DATE: 01-11-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Margaret C.
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: BNL93-28A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 282-3729
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-235-836C-114

Query Match 1.7%; Score 7; DB 3; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
    |||||
Db 196 LKREIEK 202

RESULT 31
US-09-252-991A-20165
; Sequence 20165, Application US/09252991A
; Patent No. 6551795
```


GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,798
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20165
LENGTH: 417
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20165

Query Match 1.7%; Score 7; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 ASPASTP 341
|||||
Db 369 ASPASTP 375

RESULT 32
US-08-235-836C-120
Sequence 120, Application US/08235836C
Patent No. 6248562
GENERAL INFORMATION:
APPLICANT: Dunn, John J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brookhaven National Laboratory
STREET:
CITY: Upton
STATE: NY
COUNTRY: USA
ZIP: 11973
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELEPHONE: (516) 282-7338
TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-235-836C-120

Query Match 1.7%; Score 7; DB 3; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,798
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20165
LENGTH: 417
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20165

Query Match 1.7%; Score 7; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 ASPASTP 341
|||||
Db 369 ASPASTP 375

RESULT 32
US-08-235-836C-120
Sequence 120, Application US/08235836C
Patent No. 6248562
GENERAL INFORMATION:
APPLICANT: Dunn, John J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brookhaven National Laboratory
STREET:
CITY: Upton
STATE: NY
COUNTRY: USA
ZIP: 11973
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELEPHONE: (516) 282-7338
TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-235-836C-120

Query Match 1.7%; Score 7; DB 3; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
|||||
Db 196 LKREIEK 202

RESULT 33
US-08-878-989-2
Sequence 2, Application US/08879899
Patent No. 5885803
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TBLYN0T01
CLONE: 40194
US-08-878-989-2

Query Match 1.7%; Score 7; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 QALKKIL 89
|||||
Db 247 QALKKIL 253

RESULT 34
US-09-272-796-2
Sequence 2, Application US/09272796
Patent No. 6207148

/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Corley, Neil C.
/ APPLICANT: Guegler, Karl G.
/ APPLICANT: Lal, Preeti
/ APPLICANT: Goli, Surya K.
/ APPLICANT: Shah, Purvi
/ TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
/ TITLE OF INVENTION: KINASES
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/272,796
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/878,989
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J J
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0321 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 448 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: TELYNOT01
/ CLONE: 40194
/ US-09-272-796-2

Query Match 1.7%; Score 7; DB 3; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 QALKKIL 89
| | | | |
| | | | |
Db 247 QALKKIL 253

RESULT 35
US-08-235-836C-116
/ Sequence 116, Application US/08235836C
/ Patent No. 6248562
/ GENERAL INFORMATION:
/ APPLICANT: Dunn, John J.
/ APPLICANT: Luft, Benjamin J.
/ TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
/ TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
/ NUMBER OF SEQUENCES: 144
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Brookhaven National Laboratory
/ STREET:
/ CITY: Upton
/ STATE: NY

/ COUNTRY: USA
/ ZIP: 11973
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/235,836C
/ FILING DATE: 29-APR-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/148,191
/ FILING DATE: 01-11-93
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bogosian, Margaret C.
/ REGISTRATION NUMBER: 25,324
/ REFERENCE/DOCKET NUMBER: ENL93-28A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (516) 282-7338
/ TELEFAX: (516) 282-3729
/ INFORMATION FOR SEQ ID NO: 116:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 454 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-235-836C-116

Query Match 1.7%; Score 7; DB 3; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
| | | | |
| | | | |
Db 196 LKREIEK 202

RESULT 36
US-09-328-352-4637
/ Sequence 4637, Application US/09328352
/ Patent No. 6562958
/ GENERAL INFORMATION:
/ APPLICANT: Gary L. Breton et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
/ TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: GTC99-03PA
/ CURRENT APPLICATION NUMBER: US/09/328,352
/ CURRENT FILING DATE: 1999-06-04
/ NUMBER OF SEQ ID NOS: 8252
/ SEQ ID NO 4637
/ LENGTH: 495
/ TYPE: PRT
/ ORGANISM: Acinetobacter baumannii
/ US-09-328-352-4637

Query Match 1.7%; Score 7; DB 4; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 EQALKKI 88
| | | | |
| | | | |
Db 230 EQALKKI 236

RESULT 37
US-09-134-001C-3598
/ Sequence 3598, Application US/09134001C
/ Patent No. 6380370
/ GENERAL INFORMATION:
/ APPLICANT: Lynn Doucette-Stamm et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
/ TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

```
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3598
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3598

Query Match
Best Local Similarity 1.7%; Score 7; DB 4; Length 502;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 221 SQBELK 227
Db 119 SQBELK 125

RESULT 39
US-09-344-700-4
; Sequence 4, Application US/09344700
; Patent No. 6265194
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: NOVEL SERINE-THREONINE KINASE GENE
; FILE REFERENCE: 06501/033001
; CURRENT APPLICATION NUMBER: US/09/344,700
; CURRENT FILING DATE: 1999-06-25
; EARLIER APPLICATION NUMBER: PCT/JP97/0485
; EARLIER FILING DATE: 1997-12-25
; EARLIER APPLICATION NUMBER: JP 8/357864
; EARLIER FILING DATE: 1996-12-27
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-700-4

Query Match
Best Local Similarity 1.7%; Score 7; DB 3; Length 508;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QALKKIL 89
Db 307 QALKKIL 313

RESULT 39
US-09-563-997A-4
; Sequence 4, Application US/09563997A
; Patent No. 6674437
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: NOVEL SERINE-THREONINE KINASE GENE
; FILE REFERENCE: 06501-033002
; CURRENT APPLICATION NUMBER: US/09/563,997A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/344,700
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: PCT/JP97/04855
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP 8-357864
; PRIOR FILING DATE: 1996-12-27
; NUMBER OF SEQ ID NOS: 48

; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3598
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3598

Query Match
Best Local Similarity 1.7%; Score 7; DB 4; Length 508;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QALKKIL 89
Db 307 QALKKIL 313

RESULT 40
US-09-352-991A-16994
; Sequence 16994, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16994
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-352-991A-16994

Query Match
Best Local Similarity 1.7%; Score 7; DB 4; Length 522;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 EXRGAQ 261
Db 514 EXRGAQ 520

RESULT 41
US-09-252-991A-17824
; Sequence 17824, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17824
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (224)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-17824
```

```
Query Match      1.7%; Score 7; DB 4; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 AQIOAAR 266
   |||||
Db 49 AQIOAAR 55

RESULT 42
US-09-173-053-18
; Sequence 18, Application US/09173053
; Patent No. 6451769
; GENERAL INFORMATION:
; APPLICANT: HUEBNER, Robert C.
; APPLICANT: NORMAN, Jon A.
; APPLICANT: LIANG, Xiaowu
; APPLICANT: CARNER, Kristin R.
; APPLICANT: BARBOUR, Alan G.
; APPLICANT: LUKE, Catherine J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ADMINISTERING BORRELIA DNA
; FILE REFERENCE: 454312-2440.1
; CURRENT APPLICATION NUMBER: US/09/173,053
; CURRENT FILING DATE: 1998-10-15
; PRIOR APPLICATION NUMBER: 08/663,998
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-09-173-053-18

Query Match      1.7%; Score 7; DB 4; Length 569;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
   |||||
Db 485 LKREIEK 491

RESULT 43
US-08-235-836C-122
; Sequence 122, Application US/08235836C
; Patent No. 6248562
; GENERAL INFORMATION:
; APPLICANT: Dunn, John J.
; APPLICANT: Luft, Benjamin J.
; TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
; TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brookhaven National Laboratory
; STREET:
; CITY: Upton
; STATE: NY
; COUNTRY: USA
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,836C
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,191
; FILING DATE: 01-11-93
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Bogosian, Margaret C.
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: ENL93-28A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 282-7338
; TELEFAX: (516) 282-3729
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 588 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-235-836C-122

Query Match      1.7%; Score 7; DB 3; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
   |||||
Db 196 LKREIEK 202

RESULT 44
US-09-252-991A-23497
; Sequence 23497, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23497
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23497

Query Match      1.7%; Score 7; DB 4; Length 633;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 ASPASTP 341
   |||||
Db 82 ASPASTP 88

RESULT 45
US-09-252-991A-19167
; Sequence 19167, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19167
; LENGTH: 693
; TYPE: PRT
```

```
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19167

Query Match      1.7%; Score 7; DB 4; Length 693;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GFVLGAL 18
DB      671 GFVLGAL 677

RESULT 46
US-09-433-043B-126
; Sequence 126, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 126
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-433-043B-126

Query Match      1.7%; Score 7; DB 4; Length 694;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      389 ETDEEIE 395
DB      549 ETDEEIE 555

RESULT 47
US-09-910-174B-15
; Sequence 15, Application US/09910174B
; Patent No. 6630575
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(731)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-910-174B-15

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19167

Query Match      1.7%; Score 7; DB 4; Length 693;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GFVLGAL 18
DB      671 GFVLGAL 677

RESULT 46
US-09-433-043B-126
; Sequence 126, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 126
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-433-043B-126

Query Match      1.7%; Score 7; DB 4; Length 694;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      389 ETDEEIE 395
DB      549 ETDEEIE 555

RESULT 47
US-09-910-174B-15
; Sequence 15, Application US/09910174B
; Patent No. 6630575
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(731)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-910-174B-15

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19167

Query Match      1.7%; Score 7; DB 4; Length 731;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      221 SLOEELK 227
DB      310 SLOEELK 316

RESULT 48
US-09-620-461-15
; Sequence 15, Application US/09620461
; Patent No. 6635750
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
; FILE REFERENCE: 5800-149
; CURRENT APPLICATION NUMBER: US/09/620,461
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(731)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-620-461-15

Query Match      1.7%; Score 7; DB 4; Length 731;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      221 SLOEELK 227
DB      310 SLOEELK 316

RESULT 49
US-08-249-380-2
; Sequence 2, Application US/08249380
; Patent No. 5827685
; GENERAL INFORMATION:
; APPLICANT: Lindquist, Susan
; TITLE OF INVENTION: Methods and Compositions of Genetic
; TITLE OF INVENTION: Stress Response Systems
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,380
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/710,187
; FILING DATE: 31-MAY-1991
; ATTORNEY/AGENT INFORMATION:
```

NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-249-380-2

Query Match 1.7%; Score 7; DB 2; Length 908;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLQBEL 226
|||||
Db 453 ASLQBEL 459

RESULT 50
US-09-883-134-4
Sequence 4, Application US/09883134
Patent No. 6511840
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
APPLICANT: Mathur, Daniel
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: No. 6511840el Human Kinase Proteins and Polynucleotides Encoding
FILE REFERENCE: LEX-0193-USA
CURRENT APPLICATION NUMBER: US/09/883,134
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/211,572
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/216,382
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1236
TYPE: PRT
ORGANISM: homo sapiens
US-09-883-134-4

Query Match 1.7%; Score 7; DB 4; Length 1236;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 QAAREKN 269
|||||
Db 512 QAAREKN 518

RESULT 51
US-09-181-706-2
Sequence 2, Application US/09181706
Patent No. 6130068
GENERAL INFORMATION:
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
APPLICANT: Robert F. Dubose, Richard S. Johnson
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry

STREET: 51 University St.
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181,706
FILING DATE: October 28, 1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/958,598 (converted to a
APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
FILING DATE: October 26, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-181-706-2

Query Match 1.7%; Score 7; DB 3; Length 1568;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 ALRTFFP 289
|||||
Db 1022 ALRTFFP 1028

RESULT 52
US-09-458-791-2
Sequence 2, Application US/09458791
Patent No. 6174689
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/458,791
FILING DATE: 10-Dec-1999
CLASSIFICATION: <Unknown>

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE: 28-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-458-791-2

Query Match 1.7%; Score 7; DB 3; Length 1568;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 283 ALRTFFP 289
Db 1022 ALRTFFP 1028

RESULT 53
US-09-459-066-2
; Sequence 2, Application US/09459066
; Patent No. 6187909
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA: US/09/459,066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-459-065-2

Query Match 1.7%; Score 7; DB 4; Length 1568;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 283 ALRTFFP 289
Db 1022 ALRTFFP 1028

RESULT 55
US-08-462-128-28
; Sequence 28, Application US/08462128
; Patent No. 5686059
; GENERAL INFORMATION:
; APPLICANT: Goetinck, Paul F.
; APPLICANT: Tondravi, Mehrdad
; TITLE OF INVENTION: CARTILAGE MATRIX PROTEIN AND METHODS FOR
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street
; CITY: Boston

```

```

; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,128
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/006,096
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/866,403
; FILING DATE: 10-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-462-128-28

Query Match 1.5%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 DLVFL 134
Db 1 DLVFL 6
|||||

US-08-462-128-28

RESULT 56
US-08-463-180-28
; Sequence 28, Application US/08463180
; Patent No. 5741670
; GENERAL INFORMATION:
; APPLICANT: Goetnick, Paul F.
; APPLICANT: Tondravi, Mehrdad
; TITLE OF INVENTION: CARTILAGE MATRIX PROTEIN AND METHODS FOR
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,180
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/006,096
; FILING DATE: 15-JAN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/866,403
; FILING DATE: 10-APR-1992

; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,128
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/006,096
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/866,403
; FILING DATE: 10-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-463-180-28

Query Match 1.5%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 DLVFL 134
Db 1 DLVFL 6
|||||

US-08-463-180-28

RESULT 57
US-09-171-705-77
; Sequence 77, Application US/09171705
; Patent No. 6184204
; GENERAL INFORMATION:
; APPLICANT: VERHEIJDEN, GILBERTUS F.M.
; APPLICANT: BOOTS, ANNA M.H.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/171,705
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 77
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
; US-09-171-705-77

Query Match 1.5%; Score 6; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 348 ALDLD 353
Db 3 ALDLD 8
|||||

US-09-171-705-77

RESULT 58
US-08-199-508-57
; Sequence 57, Application US/08199508
; Patent No. 5717058
; GENERAL INFORMATION:
; APPLICANT: Matthews, Maura-Ann H.
; APPLICANT: Stetler, Gary L.
; APPLICANT: Anthony-Cahill, Spencer J.
; APPLICANT: Anderson, David C.
; TITLE OF INVENTION: Modulators of Gene Expression
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 5797 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:

```


MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,508
FILING DATE: February 18, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,536
FILING DATE: February 23, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5717058ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 121 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3322
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: amino acid
TOPOLOGY: unknown to applicant
MOLECULE TYPE: peptide
HYPOTHETICAL: yes
US-08-199-508-57

Query Match 1.5%; Score 6; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 291 SEFLHS 296
Db 3 SEFLHS 8

RESULT 59
US-08-912-272-46
Sequence 46, Application US/08912272
Patent No. 6093874
GENERAL INFORMATION:
APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,272
FILING DATE: 15-AUG-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/879,827
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-067220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-026-039-46

Query Match 1.5%; Score 6; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 STGFSR 193
Db 5 STGFSR 10

RESULT 60
US-09-026-039-46
Sequence 46, Application US/09026039
Patent No. 6329567
GENERAL INFORMATION:
APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,039
FILING DATE: 19-FEB-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,272
FILING DATE: 15-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/879,827
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-067230US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-026-039-46

Query Match 1.5%; Score 6; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 STGFSR 193
| | | | |
Db 5 STGFSR 10

RESULT 61
US-09-171-705-55
; Sequence 55, Application US/09171705
; Patent No. 6184204
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIJDEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/171,705
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-55

Query Match 1.5%; Score 6; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 ALDLD 353
| | | | |
Db 8 ALDLD 13

RESULT 62
US-09-171-705-56
; Sequence 56, Application US/09171705
; Patent No. 6184204
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIJDEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/171,705
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-56

Query Match 1.5%; Score 6; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 ALDLD 353
| | | | |
Db 2 ALDLD 7

RESULT 63
US-09-205-258-1052
; Sequence 1052, Application US/09205258
; Patent No. 6525174

```
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,963
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,877
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,878
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/070,923
/ EARLIER FILING DATE: 1997-12-18
/ EARLIER APPLICATION NUMBER: 60/092,921
/ EARLIER FILING DATE: 1998-07-15
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ NUMBER OF SEQ ID NOS: 1227
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1052
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-205-258-1052

Query Match      1.5%; Score 6; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      333 PEASPA 338
Db      8 PEASPA 13

RESULT 64
US-09-205-258-1053
/ Sequence 1053, Application US/09205258
/ Patent No. 6525174
/ GENERAL INFORMATION:
/ APPLICANT: Young et al.
/ TITLE OF INVENTION: 207 Human Secreted Proteins
/ FILE REFERENCE: P2007P1
/ CURRENT APPLICATION NUMBER: US/09/205,258
/ CURRENT FILING DATE: 1998-12-04
/ EARLIER APPLICATION NUMBER: PCT/US98/11422
/ EARLIER FILING DATE: 1998-06-04
/ EARLIER APPLICATION NUMBER: 60/048,885
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,375
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,881
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,880
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,896
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,020
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,876
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,895
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,884
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,894
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,971
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,964
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,882
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,899
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,893
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,900

Query Match      1.5%; Score 6; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      333 PEASPA 338
Db      8 PEASPA 13

RESULT 65
PCT-US93-07653-1
/ Sequence 1, Application PC/TUS9307653
/ GENERAL INFORMATION:
/ APPLICANT: James Boyd
/ TITLE OF INVENTION: HEPARIN NEUTRALIZATION WITH
/ TITLE OF INVENTION: MUTIMERIC PEPTIDES
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
```

```

; ADDRESS: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07653
; FILING DATE: 19930813
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S.S.N. 07/932,456
; FILING DATE: August 17, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL T. CLARK
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00231/066W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: amino
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US93-07653-1

Query Match 1.5%; Score 6; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 ALKKIL 89
Db 3 ALKKIL 8

RESULT 66
US-08-795-430-51
; Sequence 51, Application US/08795430
; Patent No. 6130071
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,430
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FI96/00427
; FILING DATE: 01-AUG-1996
; PRIOR APPLICATION DATA:

; ADDRESSER: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07653
; FILING DATE: 19930813
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S.S.N. 07/932,456
; FILING DATE: August 17, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL T. CLARK
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00231/066W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: amino
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US93-07653-1

Query Match 1.5%; Score 6; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 KTVSGS 185
Db 3 KTVSGS 8

RESULT 67
US-09-355-700-51
; Sequence 51, Application US/09355700
; Patent No. 6361946
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; APPLICANT: Helsinki University Licensing
; APPLICANT: Alitalo, Kari (U.S. only)
; APPLICANT: Joukov, Vladimir (U.S. only)
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/355,700
; FILING DATE: 05-NOV-1994
; CLASSIFICATION: <UNKNOWN>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,430
; FILING DATE: 05-FEB-1997
; APPLICATION NUMBER: PCT/FI96/00427
; FILING DATE: 01-AUG-1996

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; APPLICATION NUMBER: 08/671,573
; FILING DATE: 28-JUN-1996
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/34140
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-355-700-51

Query Match          1.5%; Score 6; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 KTVSGS 185
Db 3 KTVSGS 8

RESULT 68
5368712-4
; Patent No. 5368712
; APPLICANT: TOMICH, JOHN;MONTAL, MAURICIO
; TITLE OF INVENTION: BIOLOGICALLY MIMETIC SYNTHETIC
; ION CHANNEL TRANSDUCERS
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/576,222
; FILING DATE: 31-AUG-1990
; SEQ ID NO:4:
; LENGTH: 23
5368712-4

Query Match          1.5%; Score 6; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 VFLLLT 136
Db 15 VFLLLT 20

RESULT 69
5516890-4
; Patent No. 5516890
; APPLICANT: TOMICH, JOHN;MONTAL, MAURICIO
; TITLE OF INVENTION: BIOLOGICALLY MIMETIC SYNTHETIC ION
; CHANNEL TRANSDUCERS AND METHODS OF MAKING THE SAME
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/312,821
; FILING DATE: 27-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 576,222
; FILING DATE: 31-AUG-1990
; APPLICANT: Jofuku, K. Diane
; APPLICANT: Okamuro, Jack K.

; APPLICATION NUMBER: 430,814
; FILING DATE: 02-NOV-1989
; SEQ ID NO:4:
; LENGTH: 23
5516890-4

Query Match          1.5%; Score 6; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 VFLLLT 136
Db 15 VFLLLT 20

RESULT 70
US-08-772-440-6
; Sequence 6, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTWD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-6

Query Match          1.5%; Score 6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VLGAIA 19
Db 20 VLGAIA 25

RESULT 71
US-08-912-272-44
; Sequence 44, Application US/08912272
; Patent No. 6093874
; GENERAL INFORMATION:
; APPLICANT: Jofuku, K. Diane
; APPLICANT: Okamuro, Jack K.
```

;; TITLE OF INVENTION: Methods for Improving Seeds
;; NUMBER OF SEQUENCES: 103
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/912,272
;; FILING DATE: 15-AUG-1997
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/879,827
;; FILING DATE: 20-JUN-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/700,152
;; FILING DATE: 20-AUG-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bastian, Kevin L.
;; REGISTRATION NUMBER: 34,774
;; REFERENCE/DOCKET NUMBER: 023070-067220US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 44:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 26 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..26
;; OTHER INFORMATION: /note= "RAP2.7 linker region"
;; US-08-912-272-44

Query Match 1.5%; Score 6; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 188 STGFSR 193
Db 20 STGFSR 25

RESULT 72
US-09-026-039-44
; Sequence 44, Application US/09026039
; Patent No. 6329567
; GENERAL INFORMATION:
; APPLICANT: Jofuku, K. Diane
; APPLICANT: Okumuro, Jack K.
; TITLE OF INVENTION: Methods for Improving Seeds
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/026,039
;; FILING DATE: 19-FEB-1998
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/912,272
;; FILING DATE: 15-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/879,827
;; FILING DATE: 20-JUN-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/700,152
;; FILING DATE: 20-AUG-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bastian, Kevin L.
;; REGISTRATION NUMBER: 34,774
;; REFERENCE/DOCKET NUMBER: 023070-067230US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 44:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 26 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..26
;; OTHER INFORMATION: /note= "RAP2.7 linker region"
;; US-09-026-039-44

Query Match 1.5%; Score 6; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 188 STGFSR 193
Db 20 STGFSR 25

RESULT 73
US-09-156-856-14
; Sequence 14, Application US/09156856A
; Patent No. 6221591
; GENERAL INFORMATION:
; APPLICANT: Aerts, Johannes M.
; TITLE OF INVENTION: Determination of a genetic risk factor for infection
; TITLE OF INVENTION: and other diseases, and detection of activated
; TITLE OF INVENTION: phagocytes
; FILE REFERENCE: Sequence 1-20
; Patent No. 6221591
; CURRENT APPLICATION NUMBER: US/09/156,856A
; CURRENT FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-156-856-14

Query Match 1.5%; Score 6; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 348 ALDLDD 353
Db 19 ALDLDD 24

```

RESULT 74
US-09-205-258-555
; Sequence 555, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897

Query Match      1.5%; Score 6; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      196 QTHSSK 201
DB      9 QTHSSK 14
      |||||
      |||||

RESULT 75
US-09-315-304B-1459
; Sequence 1459, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1459
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-315-304B-1459

Query Match      1.5%; Score 6; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      260 AQIQAA 265
DB      15 AQIQAA 20
      |||||
      |||||

RESULT 76
US-09-515-965A-1459
; Sequence 1459, Application US/09515965A

```

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; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1459
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-1459

Query Match          1.5%; Score 6; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      260 AQIQAA 265
Db      15 AQIQAA 20

RESULT 77
US-09-350-641C-1459
; Sequence 1459, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1459
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-641C-1459

Query Match          1.5%; Score 6; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      260 AQIQAA 265
Db      15 AQIQAA 20
```

```
RESULT 78
US-09-124-671-5
; Sequence 5, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hog, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/09/124,671A
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-124-671-5

Query Match          1.5%; Score 6; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 LLGEVK 38
Db      17 LLGEVK 22

RESULT 79
US-08-679-493A-170
; Sequence 170, Application US/08679493A
; Patent No. 6303295
; GENERAL INFORMATION:
; APPLICANT: Taylor, Ethan W.
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
; FILE REFERENCE: 55-95
; CURRENT APPLICATION NUMBER: US/08/679,493A
; CURRENT FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 60/001203
; PRIOR FILING DATE: 1995-07-14
; PRIOR APPLICATION NUMBER: 60/003,112
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 170
; LENGTH: 46
; TYPE: PRT
; ORGANISM: macaque
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(46)
; OTHER INFORMATION: X is selenocysteine.
US-08-679-493A-170

Query Match          1.5%; Score 6; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      222 LQELK 227
Db      14 LQELK 19

RESULT 80
US-09-205-258-399
; Sequence 399, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
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; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: FCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,871
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER FILING DATE: 1997-06-06
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; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 399
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (47)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-399

Query Match 1.5%; Score 6; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy 333 PEASPA 338
Db 40 PEASPA 45
|||||

RESULT 81
US-09-621-976-6873
; Sequence 6873, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6873
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 5
; OTHER INFORMATION: Xaa = Asp,Glu
US-09-621-976-6873

Query Match 1.5%; Score 6; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy 336 SPASTP 341
Db 8 SPASTP 13
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RESULT 82
US-09-167-681-43
; Sequence 43, Application US/09167681A
; Patent No. 6265561
; GENERAL INFORMATION:
; APPLICANT: Weinshilboum, M.D., Richard M.
; APPLICANT: Raftogiannis, Rebecca B.
; APPLICANT: Wood, Thomas C.
; APPLICANT: Ottewill, Diane M.
; TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
; FILE REFERENCE: 07039/118001
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; CURRENT APPLICATION NUMBER: US/09/167,681A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-167-681-43

Query Match      1.5%; Score 6; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      325 LMVHNT 330
Db      24 LMVHNT 29
      |||||

RESULT 83
US-08-936-165A-291
; Sequence 291, Application US/08936165A
; Patent No. 6348582
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Burnham, Martin
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Lonetto, Michael
; APPLICANT: Nicholas, Richard
; APPLICANT: Pratt, Julie
; APPLICANT: Reichard, Richard
; APPLICANT: Rosenberg, Martin
; APPLICANT: Ward, Judith
; TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
; TITLE OF INVENTION: Polypeptides and Their Uses
; NUMBER OF SEQUENCES: 534
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,165A
; FILING DATE: 24-SEP-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/027,032
; FILING DATE: 24-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50549
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 291:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-936-165A-291

Query Match      1.5%; Score 6; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      325 LMVHNT 330
Db      24 LMVHNT 29
      |||||

Query Match      1.5%; Score 6; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      320 VDNLT 325
Db      47 VDNLT 52
      |||||

RESULT 84
US-09-134-000C-4727
; Sequence 4727, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4727
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4727

Query Match      1.5%; Score 6; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      167 VVANLG 172
Db      43 VVANLG 48
      |||||

RESULT 85
US-09-716-129-52
; Sequence 52, Application US/09716129
; Patent No. 6632920
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P2025P1
; CURRENT APPLICATION NUMBER: US/09/716,129
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/076,053
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,057
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,052
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,054
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,051
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (66)
; OTHER INFORMATION: Xaa equals stop translation
US-09-716-129-52

Query Match      1.5%; Score 6; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 165 PLVAVN 170
Db 17 PLVAVN 22

RESULT 86
US-09-149-476-430
; Sequence 430, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
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; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
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RESULT 87
US-09-308-003-15
; Sequence 15, Application US/09308003
; Patent No. 6326170
; GENERAL INFORMATION:
; APPLICANT: Burnham, Martin K. R.
; APPLICANT: Lonetto, Michael A.
; APPLICANT: Warren, Patrick V.
; TITLE OF INVENTION: NOVEL PROKARYOTIC POLYNUCLEOTIDES,
; FILE REFERENCE: GM10093
; CURRENT APPLICATION NUMBER: US/09/308,003
; CURRENT FILING DATE: 1999-05-10
; EARLIER APPLICATION NUMBER: 60/058,710
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-308-003-15
Query Match 1.5%; Score 6; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 320 VDNLT 325
DB 50 VDNLT 55
RESULT 88
US-08-280-443-25
; Sequence 25, Application US/08280443
; Patent No. 5643778
; GENERAL INFORMATION:
; APPLICANT: Nishikura, Kazuko
; TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/280,443
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,794
; FILING DATE: 17-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST49AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
Query Match 1.5%; Score 6; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 367 DKRSKA 372
DB 42 DKRSKA 47

US-08-280-443-25

Query Match 1.5%; Score 6; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 EQALKK 87
DB 64 EQALKK 69

RESULT 89

US-08-457-459-25

Sequence 25, Application US/08457459
Patent No. 5677428

GENERAL INFORMATION:
APPLICANT: Nishikura, Kazuko
TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,459
FILING DATE: 25-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,459
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST49CUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-457-459-25

Query Match 1.5%; Score 6; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 EQALKK 87
DB 64 EQALKK 69

RESULT 90

US-08-555-678-25

Sequence 25, Application US/08555678
Patent No. 5763174

GENERAL INFORMATION:
APPLICANT: Nishikura, Kazuko
TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,678
FILING DATE: 25-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,459
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST49CUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-555-678-25

Query Match 1.5%; Score 6; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 EQALKK 87
DB 64 EQALKK 69

RESULT 91

PCT-US95-02275-25

Sequence 25, Application PC/TUS9502275

GENERAL INFORMATION:
APPLICANT: Wistar Institute of Anatomy & Biology
TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,678
FILING DATE: 25-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,459
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST49CUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-555-678-25

Query Match 1.5%; Score 6; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 EQALKK 87
DB 64 EQALKK 69

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; APPLICATION NUMBER: PCT/US95/02275
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/280,443
; FILING DATE: 25-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,794
; FILING DATE: 17-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST49BPCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US95-02275-25

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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      82 EQALKK 87
Db      64 EQALKK 69

RESULT 92
US-09-621-976-6090
; Sequence 6090, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6090
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6090

Query Match      1.5%; Score 6; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      130 LVFLLL 135
Db      64 LVFLLL 69

RESULT 93
US-09-489-039A-13015
; Sequence 13015, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A

; APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13015
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13015

Query Match      1.5%; Score 6; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      130 LVFLLL 135
Db      57 LVFLLL 62

RESULT 94
US-07-881-075-16
; Sequence 16, Application US/07881075
; Patent No. 5444149
; GENERAL INFORMATION:
; APPLICANT: KEENE, JACK D.
; APPLICANT: KING, PETER H.
; APPLICANT: LEVINE, TODD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
; TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
; TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/881,075
; FILING DATE: 19920511
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5444149man P.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 714-154-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-07-881-075-16

Query Match      1.5%; Score 6; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      223 QEELKS 228
Db      13 QEELKS 18
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RESULT 95
US-08-120-827-16
; Sequence 16, Application US/08120827
; Patent No. 5525495
; GENERAL INFORMATION:
; APPLICANT: KEENE, JACK D.
; APPLICANT: KING, PETER H.
; APPLICANT: LEVINE, TODD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
; TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
; TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/120,827
; FILING DATE: 15-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5525495man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 714-158-0 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-120-827-16

Query Match 1.5%; Score 6; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 QEELKS 228
Db 13 QEELKS 18

RESULT 96
US-08-478-675-16
; Sequence 16, Application US/08478675
; Patent No. 5773246
; GENERAL INFORMATION:
; APPLICANT: KEENE, JACK D.
; APPLICANT: KING, PETER H.
; APPLICANT: LEVINE, TODD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
; TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
; TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.

Query Match 1.5%; Score 6; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 QEELKS 228
Db 13 QEELKS 18

RESULT 97
US-09-621-976-3983
; Sequence 3983, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3983
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -24...-1
US-09-621-976-3983

Query Match 1.5%; Score 6; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 LLLTPS 138
Db 53 LLLTPS 58

RESULT 98
US-08-851-843A-220
; Sequence 220, Application US/08851843A
```

; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-00293005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-851-843A-220

Query Match 1.5%; Score 6; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 336 SPASTP 341
Db 44 SPASTP 49

RESULT 99
US-08-974-549A-339
; Sequence 339, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-00261005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-974-549A-339

Query Match 1.5%; Score 6; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 336 SPASTP 341
Db 44 SPASTP 49

Db 44 SPASTP 49

Search completed: April 16, 2004, 10:21:28
Job time : 31 secs

RESULT 100
US-08-854-050-220
; Sequence 220, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-854-050-220

Query Match 1.5%; Score 6; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.2e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 336 SPASTP 341
Db 44 SPASTP 49

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OM protein - protein search, using sw model

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(without alignments)
1958.677 Million cell updates/sec

Title: US-10-063-523-22

Perfect score: 409
Sequence: 1 MEGESTAVLSGFVGLALAF.....TDSEIEKMKGFGRYSRPTF 409

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Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 6

Total number of hits satisfying chosen parameters: 8027

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

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- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	409	100.0	409	4	Aau29090 Human PRO
3	409	100.0	409	4	Aab87536 Human PRO
4	409	100.0	409	4	Aab65189 Human PRO
5	409	100.0	409	5	Abg95861 Human sec
6	409	100.0	409	6	Abu58466 Human PRO
7	409	100.0	409	6	Abu88014 Novel hum
8	409	100.0	409	6	Abu84329 Human sec
9	409	100.0	409	6	Abf66203 Human sec
10	409	100.0	409	6	Abf65593 Human sec
11	409	100.0	409	6	Abu99533 Human sec
12	409	100.0	409	6	Abu58004 Human PRO
13	409	100.0	409	6	Abu59082 Novel hum
14	409	100.0	409	6	Abu82594 Human sec
15	409	100.0	409	6	Abu82722 Human PRO
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17	409	100.0	409	6	Abf68142 Human sec
18	409	100.0	409	6	Abu60513 Human sec
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25	409	100.0	409	6	Abu13895 Human PRO

26	409	100.0	409	6	ABU85644	Human PRO
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30	409	100.0	409	6	ABU89418	Human PRO
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33	409	100.0	409	6	ABU80500	Human PRO
34	409	100.0	409	6	ABU72480	Novel hum
35	409	100.0	409	6	ABU90886	Novel hum
36	409	100.0	409	6	ABO33945	Human sec
37	409	100.0	409	6	ABR99418	Human sec
38	409	100.0	409	6	ABR98808	Human sec
39	409	100.0	409	6	ABO16331	Human sec
40	409	100.0	409	6	ABR92231	Human sec
41	409	100.0	409	6	ABO18872	Human sec
42	409	100.0	409	6	ABR78293	Human sec
43	409	100.0	409	6	ABU71562	Novel hum
44	409	100.0	409	6	ABU85029	Novel hum
45	409	100.0	409	6	ABO00168	Novel hum
46	409	100.0	409	6	ABO11500	Human sec
47	409	100.0	409	6	ABO02145	Human sec
48	409	100.0	409	6	ABU88719	Novel hum
49	409	100.0	409	6	ABU83414	Human sec
50	409	100.0	409	6	ABO06215	Novel hum
51	409	100.0	409	6	ABR59251	Human sec
52	409	100.0	409	6	ABO09313	Human sec
53	409	100.0	409	6	ABO19177	Novel hum
54	409	100.0	409	6	ABO11195	Human sec
55	409	100.0	409	6	ABR66813	Human sec
56	409	100.0	409	6	ABO16026	Human sec
57	409	100.0	409	6	ABO13732	Human sec
58	409	100.0	409	6	ABU71516	Human sec
59	409	100.0	409	6	ABU65635	Human sec
60	409	100.0	409	6	ABO07483	Human PRO
61	409	100.0	409	6	ABO03670	Human sec
62	409	100.0	409	6	ABR67118	Human sec
63	409	100.0	409	6	ABO15721	Human sec
64	409	100.0	409	6	ABU56002	Human sec
65	409	100.0	409	6	ABU72297	Human PRO
66	409	100.0	409	6	ABU65330	Human PRO
67	409	100.0	409	6	ABU95275	Novel hum
68	409	100.0	409	6	ABU71178	Human PRO
69	409	100.0	409	6	ABO07788	Human PRO
70	409	100.0	409	6	ABR70029	Human sec
71	409	100.0	409	6	ABR69362	Human sec
72	409	100.0	409	6	ABO01503	Human PRO
73	409	100.0	409	6	ABU81305	Human PRO
74	409	100.0	409	6	ABR60102	Human sec
75	409	100.0	409	6	ABU90970	Human PRO
76	409	100.0	409	6	ABR67837	Human sec
77	409	100.0	409	6	ABR65225	Human sec
78	409	100.0	409	6	ABR68447	Human sec
79	409	100.0	409	6	ABR71859	Human sec
80	409	100.0	409	6	ABU59229	Human sec
81	409	100.0	409	6	ABU85339	Human sec
82	409	100.0	409	6	ABU89029	Human PRO
83	409	100.0	409	6	ABU83109	Human sec
84	409	100.0	409	6	ABU94965	Novel hum
85	409	100.0	409	6	ABU90513	Novel hum
86	409	100.0	409	6	ABU84024	Human sec
87	409	100.0	409	6	ABU93675	Novel hum
88	409	100.0	409	6	ABO25926	Human PRO
89	409	100.0	409	6	ABR64920	Human sec
90	409	100.0	409	6	ABO27291	Human sec
91	409	100.0	409	6	ABR68752	Human sec
92	409	100.0	409	6	ABO65568	Human sec
93	409	100.0	409	6	ABR99113	Human PRO
94	409	100.0	409	6	ABU56997	Novel hum
95	409	100.0	409	6	ABU85949	Novel hum
96	409	100.0	409	6	ABU82236	Novel hum
97	409	100.0	409	6	ABU87247	Human PRO
98	409	100.0	409	6	ABU83719	Human sec

99	409	100.0	409	6	ABO08093	Human	PRO	172	409	100.0	409	6	ABR90316	Human	sec
100	409	100.0	409	6	ABU92486	Human	sec	173	409	100.0	409	6	ABM17230	Human	sec
101	409	100.0	409	6	ABU81804	Novel	hum	174	409	100.0	409	6	ABR94976	Human	sec
102	409	100.0	409	6	ABU65968	Novel	hum	175	409	100.0	409	6	ABR95281	Human	sec
103	409	100.0	409	6	ABU81156	Human	sec	176	409	100.0	409	6	ABD17079	Human	tra
104	409	100.0	409	6	ABR59797	Human	sec	177	409	100.0	409	6	ABO21519	Human	sec
105	409	100.0	409	6	ABU93985	Novel	hum	178	409	100.0	409	6	ABR97783	Human	sec
106	409	100.0	409	6	ABU99838	Novel	hum	179	409	100.0	409	6	ABR87571	Human	sec
107	409	100.0	409	6	ABR66508	Human	sec	180	409	100.0	409	6	ABM77612	Human	sec
108	409	100.0	409	6	ABR90926	Human	sec	181	409	100.0	409	6	ABM27842	Human	sec
109	409	100.0	409	6	ABO53271	Novel	hum	182	409	100.0	409	6	ABM06123	Human	sec
110	409	100.0	409	6	ABU58935	Human	sec	183	409	100.0	409	6	ABM03629	Human	sec
111	409	100.0	409	6	ABU94353	Human	PRO	184	409	100.0	409	6	ABM35080	Human	sec
112	409	100.0	409	6	ABU79235	Human	PRO	185	409	100.0	409	6	ABM26317	Human	sec
113	409	100.0	409	6	ABU86564	Human	sec	186	409	100.0	409	6	ABO48099	Human	sec
114	409	100.0	409	6	ABU86869	Novel	hum	187	409	100.0	409	6	ABR92841	Human	sec
115	409	100.0	409	6	ABU94658	Human	PRO	188	409	100.0	409	6	ABO24602	Human	sec
116	409	100.0	409	6	ABO04585	Human	PRO	189	409	100.0	409	6	ADA37669	Human	sec
117	409	100.0	409	6	ABR70334	Human	sec	190	409	100.0	409	6	ABM11613	Human	sec
118	409	100.0	409	6	ABU92313	Novel	hum	191	409	100.0	409	6	ABM02714	Human	sec
119	409	100.0	409	6	ABU98499	Human	PRO	192	409	100.0	409	6	ABM16010	Human	sec
120	409	100.0	409	6	ABR65898	Human	sec	193	409	100.0	409	6	ABO27571	Human	sec
121	409	100.0	409	6	ABR64615	Human	sec	194	409	100.0	409	6	ABM29062	Human	sec
122	409	100.0	409	6	ABU59378	Novel	hum	195	409	100.0	409	6	ABM07038	Human	sec
123	409	100.0	409	6	ABU79540	Human	PRO	196	409	100.0	409	6	ABM21132	Human	sec
124	409	100.0	409	6	ABU92931	Human	sec	197	409	100.0	409	6	ABM09478	Human	sec
125	409	100.0	409	6	ABU95890	Human	PRO	198	409	100.0	409	6	ABO41348	Human	sec
126	409	100.0	409	6	ABU91110	Novel	hum	199	409	100.0	409	6	ABO36163	Human	PRO
127	409	100.0	409	6	ABU90203	Novel	hum	200	409	100.0	409	6	ABO43692	Human	PRO
128	409	100.0	409	6	ABO09618	Human	sec	201	409	100.0	409	6	ABM76392	Human	sec
129	409	100.0	409	6	ABO10890	Human	sec	202	409	100.0	409	6	ABM76088	Human	sec
130	409	100.0	409	6	ABR70944	Human	sec	203	409	100.0	409	6	ABM25707	Human	sec
131	409	100.0	409	6	ABU98273	Novel	hum	204	409	100.0	409	6	ABM26012	Human	sec
132	409	100.0	409	6	ABU87552	Human	PRO	205	409	100.0	409	6	ADA21355	Human	sec
133	409	100.0	409	6	ABU91420	Human	PRO	206	409	100.0	409	6	ABO03365	Human	sec
134	409	100.0	409	6	ABU89278	Novel	hum	207	409	100.0	409	6	ABO02450	Human	sec
135	409	100.0	409	6	ABU84634	Human	sec	208	409	100.0	409	6	ABO44249	Human	sec
136	409	100.0	409	6	ABR69724	Human	sec	209	409	100.0	409	6	ABR90621	Human	sec
137	409	100.0	409	6	ABU80101	Human	PRO	210	409	100.0	409	6	ABR73689	Human	sec
138	409	100.0	409	6	ABU82485	Novel	hum	211	409	100.0	409	6	ABO16941	Human	sec
139	409	100.0	409	6	ABU92144	Novel	hum	212	409	100.0	409	6	ABR94366	Human	sec
140	409	100.0	409	6	ABU93370	Human	PRO	213	409	100.0	409	6	ABR75873	Human	sec
141	409	100.0	409	6	ABO09923	Human	sec	214	409	100.0	409	6	ABR71249	Human	sec
142	409	100.0	409	6	ABO09008	Human	sec	215	409	100.0	409	6	ABR93146	Human	sec
143	409	100.0	409	6	ABU96449	Human	PRO	216	409	100.0	409	6	ABR93451	Human	sec
144	409	100.0	409	6	ABU10850	Human	PRO	217	409	100.0	409	6	ADA10142	Human	sec
145	409	100.0	409	6	ABU10576	Human	sec	218	409	100.0	409	6	ABR87876	Human	sec
146	409	100.0	409	6	ABU81602	Novel	hum	219	409	100.0	409	6	ABO27876	Human	sec
147	409	100.0	409	6	ABU72119	Human	PRO	220	409	100.0	409	6	ABO30011	Human	sec
148	409	100.0	409	6	ABU95585	Human	PRO	221	409	100.0	409	6	ABO33220	Human	PRO
149	409	100.0	409	6	ABU96794	Novel	hum	222	409	100.0	409	6	ABM04908	Human	sec
150	409	100.0	409	6	ABR70639	Human	sec	223	409	100.0	409	6	ABM08868	Human	sec
151	409	100.0	409	6	ABO04990	Novel	hum	224	409	100.0	409	6	ABO36468	Human	sec
152	409	100.0	409	6	ABO08398	Human	sec	225	409	100.0	409	6	ABO35553	Human	PRO
153	409	100.0	409	6	ABR89541	Human	sec	226	409	100.0	409	6	ABO39518	Human	sec
154	409	100.0	409	6	ABR34055	Human	PRO	227	409	100.0	409	6	ABM10393	Human	sec
155	409	100.0	409	6	ABO05605	Human	sec	228	409	100.0	409	6	ABM11918	Human	sec
156	409	100.0	409	6	ABR73994	Human	sec	229	409	100.0	409	6	ABO52064	Human	PRO
157	409	100.0	409	6	ABR95586	Human	sec	230	409	100.0	409	6	ABO52369	Human	PRO
158	409	100.0	409	6	ABR80883	Human	sec	231	409	100.0	409	6	ADA19884	Novel	hum
159	409	100.0	409	6	ABR81188	Human	sec	232	409	100.0	409	6	ABO23687	Human	sec
160	409	100.0	409	6	ABM00884	Human	sec	233	409	100.0	409	6	ABD17267	Human	tra
161	409	100.0	409	6	ABR8486	Human	sec	234	409	100.0	409	6	ADA17686	Human	PRO
162	409	100.0	409	6	ABM77307	Human	sec	235	409	100.0	409	6	ABR97173	Human	sec
163	409	100.0	409	6	ABO28791	Human	sec	236	409	100.0	409	6	ABR86961	Human	sec
164	409	100.0	409	6	ABO31536	Human	sec	237	409	100.0	409	6	ABM11003	Human	sec
165	409	100.0	409	6	ABM07953	Human	sec	238	409	100.0	409	6	ABM28147	Human	sec
166	409	100.0	409	6	ABO40433	Human	sec	239	409	100.0	409	6	ABO32146	Human	sec
167	409	100.0	409	6	ABO35858	Human	PRO	240	409	100.0	409	6	ABM15273	Human	sec
168	409	100.0	409	6	ABO43997	Human	PRO	241	409	100.0	409	6	ABM06428	Human	sec
169	409	100.0	409	6	ADA77886	Human	sec	242	409	100.0	409	6	ABM04239	Human	sec
170	409	100.0	409	6	ABM24792	Human	sec	243	409	100.0	409	6	ABM22352	Human	sec
171	409	100.0	409	6	ABO03060	Human	sec	244	409	100.0	409	6	ABM07648	Human	sec

245	409	100.0	409	100.0	409	6	ABO40738	Human sec	318	409	100.0	409	6	ABO37078	Human sec
246	409	100.0	409	100.0	409	6	ABM35385	Human sec	319	409	100.0	409	6	ABO41653	Human sec
247	409	100.0	409	100.0	409	6	ABM33148	Human sec	320	409	100.0	409	6	ABO35248	Human PRO
248	409	100.0	409	100.0	409	6	ABO32674	Human PRO	321	409	100.0	409	6	ABM25097	Human sec
249	409	100.0	409	100.0	409	6	ABO50234	Human sec	322	409	100.0	409	6	ABO47489	Human sec
250	409	100.0	409	100.0	409	6	ABU99228	Human sec	323	409	100.0	409	6	ABO47794	Human sec
251	409	100.0	409	100.0	409	6	ABO04280	Human sec	324	409	100.0	409	6	ABO48404	Human sec
252	409	100.0	409	100.0	409	6	ABO05910	Human sec	325	409	100.0	409	6	ABO51454	Human PRO
253	409	100.0	409	100.0	409	6	ABM18450	Human sec	326	409	100.0	409	6	ABO51759	Human PRO
254	409	100.0	409	100.0	409	6	ADA27794	Human sec	327	409	100.0	409	6	ABO50539	Human sec
255	409	100.0	409	100.0	409	6	ABR97478	Human sec	328	409	100.0	409	6	ABR79663	Human sec
256	409	100.0	409	100.0	409	6	ABR80578	Human sec	329	409	100.0	409	6	ABM16925	Human sec
257	409	100.0	409	100.0	409	6	ABM01189	Human sec	330	409	100.0	409	6	ABO17957	Human sec
258	409	100.0	409	100.0	409	6	ABR88791	Human sec	331	409	100.0	409	6	ABO20909	Human sec
259	409	100.0	409	100.0	409	6	ABM13443	Human sec	332	409	100.0	409	6	ABR96868	Human sec
260	409	100.0	409	100.0	409	6	ABM20827	Human sec	333	409	100.0	409	6	ADA38599	Human sec
261	409	100.0	409	100.0	409	6	ABO41958	Human sec	334	409	100.0	409	6	ABM12223	Human sec
262	409	100.0	409	100.0	409	6	ABO42568	Human sec	335	409	100.0	409	6	ABM16315	Human sec
263	409	100.0	409	100.0	409	6	ABM10088	Human sec	336	409	100.0	409	6	ABM24182	Human sec
264	409	100.0	409	100.0	409	6	ABO38603	Human sec	337	409	100.0	409	6	ABM14663	Human sec
265	409	100.0	409	100.0	409	6	ABM32843	Human sec	338	409	100.0	409	6	ABM04544	Human sec
266	409	100.0	409	100.0	409	6	ABM22657	Human sec	339	409	100.0	409	6	ABM06733	Human sec
267	409	100.0	409	100.0	409	6	ABM74868	Human sec	340	409	100.0	409	6	ABM09173	Human sec
268	409	100.0	409	100.0	409	6	ADA79678	Human sec	341	409	100.0	409	6	ABO39213	Human sec
269	409	100.0	409	100.0	409	6	ABR96258	Human sec	342	409	100.0	409	6	ABM75478	Human sec
270	409	100.0	409	100.0	409	6	ABM02409	Human sec	343	409	100.0	409	6	ABM25402	Human sec
271	409	100.0	409	100.0	409	6	ABR86331	Human sec	344	409	100.0	409	6	ABM19912	Human sec
272	409	100.0	409	100.0	409	6	ABR86656	Human sec	345	409	100.0	409	6	ABO46818	Human PRO
273	409	100.0	409	100.0	409	6	ABM16620	Human sec	346	409	100.0	409	6	ABO47123	Human PRO
274	409	100.0	409	100.0	409	6	ABM29672	Human sec	347	409	100.0	409	6	ADA83203	Human sec
275	409	100.0	409	100.0	409	6	ABO29096	Human sec	348	409	100.0	409	6	ABR71554	Human sec
276	409	100.0	409	100.0	409	6	ABM23877	Human sec	349	409	100.0	409	6	ABR72164	Human sec
277	409	100.0	409	100.0	409	6	ABM23267	Human sec	350	409	100.0	409	6	ABR98503	Human sec
278	409	100.0	409	100.0	409	6	ABM22047	Human sec	351	409	100.0	409	6	ABO06873	Human sec
279	409	100.0	409	100.0	409	6	ABO37688	Human sec	352	409	100.0	409	6	ABR84826	Human sec
280	409	100.0	409	100.0	409	6	ABM28452	Human sec	353	409	100.0	409	6	ABR73384	Human sec
281	409	100.0	409	100.0	409	6	ABM28757	Human sec	354	409	100.0	409	6	ABR76478	Human sec
282	409	100.0	409	100.0	409	6	ABM66401	Human sec	355	409	100.0	409	6	ABR73079	Human sec
283	409	100.0	409	100.0	409	6	ABM75783	Human sec	356	409	100.0	409	6	ABM18145	Human sec
284	409	100.0	409	100.0	409	6	ABM34063	Human sec	357	409	100.0	409	6	ABO20604	Human sec
285	409	100.0	409	100.0	409	6	ABM34368	Human sec	358	409	100.0	409	6	ABO25347	Human PRO
286	409	100.0	409	100.0	409	6	ABO20299	Human sec	359	409	100.0	409	6	ABO25652	Human PRO
287	409	100.0	409	100.0	409	6	ABO21214	Human sec	360	409	100.0	409	6	ABR94061	Human sec
288	409	100.0	409	100.0	409	6	ABO22129	Human sec	361	409	100.0	409	6	ADA92720	Human sec
289	409	100.0	409	100.0	409	6	ADA20056	Novel hum	362	409	100.0	409	6	ABR79968	Human sec
290	409	100.0	409	100.0	409	6	ABO34177	Human sec	363	409	100.0	409	6	ABM11308	Human sec
291	409	100.0	409	100.0	409	6	ABR96563	Human sec	364	409	100.0	409	6	ABO32915	Human PRO
292	409	100.0	409	100.0	409	6	ADA94374	Human sec	365	409	100.0	409	6	ABO30621	Human sec
293	409	100.0	409	100.0	409	6	ABR85741	Human sec	366	409	100.0	409	6	ABO30926	Human sec
294	409	100.0	409	100.0	409	6	ABR99723	Human sec	367	409	100.0	409	6	ABM27232	Human sec
295	409	100.0	409	100.0	409	6	ABM00274	Human sec	368	409	100.0	409	6	ABM29977	Human sec
296	409	100.0	409	100.0	409	6	ABM00579	Human sec	369	409	100.0	409	6	ABM05513	Human sec
297	409	100.0	409	100.0	409	6	ABO29706	Human sec	370	409	100.0	409	6	ABM15578	Human sec
298	409	100.0	409	100.0	409	6	ABM23572	Human sec	371	409	100.0	409	6	ABM08563	Human sec
299	409	100.0	409	100.0	409	6	ABM29367	Human sec	372	409	100.0	409	6	ABO42263	Human sec
300	409	100.0	409	100.0	409	6	ABO38298	Human sec	373	409	100.0	409	6	ABO37993	Human sec
301	409	100.0	409	100.0	409	6	ABO45598	Human PRO	374	409	100.0	409	6	ABO45903	Human PRO
302	409	100.0	409	100.0	409	6	ABM20522	Human sec	375	409	100.0	409	6	ABM66706	Human sec
303	409	100.0	409	100.0	409	6	ADA81405	Human sec	376	409	100.0	409	6	ABD20246	Human sec
304	409	100.0	409	100.0	409	6	ABO16636	Human sec	377	409	100.0	409	6	ABM19607	Human sec
305	409	100.0	409	100.0	409	6	ABO18262	Human sec	378	409	100.0	409	6	ABO49319	Human sec
306	409	100.0	409	100.0	409	6	ABO22689	Human PRO	379	409	100.0	409	6	ABO49624	Human sec
307	409	100.0	409	100.0	409	6	ABO22994	Human PRO	380	409	100.0	409	6	ADA78498	Human sec
308	409	100.0	409	100.0	409	6	ABR92536	Human sec	381	409	100.0	409	6	ABR88181	Human sec
309	409	100.0	409	100.0	409	6	ABR81493	Human sec	382	409	100.0	409	6	ADA00353	Human sec
310	409	100.0	409	100.0	409	6	ABM77917	Human sec	383	409	100.0	409	6	ABM26927	Human sec
311	409	100.0	409	100.0	409	6	ABR9706	Human sec	384	409	100.0	409	6	ABM03324	Human sec
312	409	100.0	409	100.0	409	6	ABM26622	Human sec	385	409	100.0	409	7	ABO39823	Human sec
313	409	100.0	409	100.0	409	6	ABM13748	Human sec	386	409	100.0	409	7	ABO49929	Human sec
314	409	100.0	409	100.0	409	6	ABO28486	Human sec	387	409	100.0	409	7	ABO50844	Human sec
315	409	100.0	409	100.0	409	6	ABO30316	Human sec	388	409	100.0	409	7	ABO05300	Human sec
316	409	100.0	409	100.0	409	6	ABM07343	Human sec	389	409	100.0	409	7	ABR74604	Human sec
317	409	100.0	409	100.0	409	6	ABM03934	Human sec	390	409	100.0	409	7	ABR77083	Human sec

391	409	100.0	409	7	ABM17840	Human sec
392	409	100.0	409	7	ABR95891	Human sec
393	409	100.0	409	7	ABO21824	Human sec
394	409	100.0	409	7	ABO19994	Human sec
395	409	100.0	409	7	ABO24297	Human sec
396	409	100.0	409	7	ABR86046	Human sec
397	409	100.0	409	7	ABM10698	Human sec
398	409	100.0	409	7	ABM76697	Human sec
399	409	100.0	409	7	ABR89401	Human sec
400	409	100.0	409	7	ABR8401	Human sec
401	409	100.0	409	7	ABM12528	Human sec
402	409	100.0	409	7	ABM05818	Human sec
403	409	100.0	409	7	ABO34943	Human PRO
404	409	100.0	409	7	ABM03019	Human sec
405	409	100.0	409	7	ABM13997	Human sec
406	409	100.0	409	7	ABM13502	Human sec
407	409	100.0	409	7	ABO46513	Human PRO
408	409	100.0	409	7	ABO49014	Human sec
409	409	100.0	409	7	ABR69057	Human sec
410	409	100.0	409	7	ABR89096	Human sec
411	409	100.0	409	7	ABR72469	Human sec
412	409	100.0	409	7	ABR74299	Human sec
413	409	100.0	409	7	ABO18567	Human sec
414	409	100.0	409	7	ABR80273	Human sec
415	409	100.0	409	7	ABM01494	Human sec
416	409	100.0	409	7	ABR87266	Human sec
417	409	100.0	409	7	ABM12833	Human sec
418	409	100.0	409	7	ABM30587	Human sec
419	409	100.0	409	7	ABM24487	Human sec
420	409	100.0	409	7	ABO29401	Human sec
421	409	100.0	409	7	ABO31231	Human sec
422	409	100.0	409	7	ABM14358	Human sec
423	409	100.0	409	7	ABM09783	Human sec
424	409	100.0	409	7	ABO38908	Human sec
425	409	100.0	409	7	ABM34673	Human sec
426	409	100.0	409	7	ABO51149	Human sec
427	409	100.0	409	7	ABO03975	Human sec
428	409	100.0	409	7	ABO10445	Human PRO
429	409	100.0	409	7	ABO53141	Human sec
430	409	100.0	409	7	ABR77688	Human sec
431	409	100.0	409	7	ABR78898	Human sec
432	409	100.0	409	7	ABO23992	Human sec
433	409	100.0	409	7	ABR93756	Human sec
434	409	100.0	409	7	ABM01799	Human sec
435	409	100.0	409	7	ABM78222	Human sec
436	409	100.0	409	7	ABR90011	Human sec
437	409	100.0	409	7	ADA22281	Human sec
438	409	100.0	409	7	ABM27537	Human sec
439	409	100.0	409	7	ABM31338	Human sec
440	409	100.0	409	7	ABO31841	Human sec
441	409	100.0	409	7	ABM14053	Human sec
442	409	100.0	409	7	ABM08258	Human sec
443	409	100.0	409	7	ABO40128	Human sec
444	409	100.0	409	7	ABM74563	Human sec
445	409	100.0	409	7	ABM33758	Human sec
446	409	100.0	409	7	ABM20217	Human sec
447	409	100.0	409	7	ABO48709	Human sec
448	409	100.0	409	7	ABO22511	Human sec
449	409	100.0	409	7	ABR72774	Human sec
450	409	100.0	409	7	ABO15416	Human sec
451	409	100.0	409	7	ABR85131	Human sec
452	409	100.0	409	7	ABO15111	Human sec
453	409	100.0	409	7	ABO17246	Human sec
454	409	100.0	409	7	ABM17535	Human sec

CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
XX
SQ Sequence 409 AA;

Query Match 100.0%; Score 409; DB 3; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGSGFVLGALAFQHLNLTSDTEGFLGKGEAKNSITDSQMDVVEVYITD 60
DB 1 MEGESTSAVLGSGFVLGALAFQHLNLTSDTEGFLGKGEAKNSITDSQMDVVEVYITD 60
QY 61 IQYIIPCQLRPFYNSGGEVNEQALKLISNVKKNVGVGKFRHSDQIMTFRRLHKN 120
DB 61 IQYIIPCQLRPFYNSGGEVNEQALKLISNVKKNVGVGKFRHSDQIMTFRRLHKN 120
QY 121 LQEHFSNQLDVLFLLTPTSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180
DB 121 LQEHFSNQLDVLFLLTPTSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180
QY 181 TVSGSCMTGFRVAVOTHSKFFEDGSLKEVHKINEMVYASLOELKSI CKKVEDSEAV 240
DB 181 TVSGSCMTGFRVAVOTHSKFFEDGSLKEVHKINEMVYASLOELKSI CKKVEDSEAV 240
QY 241 DKLVKDVNKLKREIEKRGQAQQAAREKNIQKDPENIFLQALRTFFPNSEFLHSCVMS 300
DB 241 DKLVKDVNKLKREIEKRGQAQQAAREKNIQKDPENIFLQALRTFFPNSEFLHSCVMS 300
QY 301 LKNRHSKSSCNYNHLDVVDNLTLVHTDIPASPASTPQIIKHKALDLDLRWQFKRS 360
DB 301 LKNRHSKSSCNYNHLDVVDNLTLVHTDIPASPASTPQIIKHKALDLDLRWQFKRS 360
QY 361 RLIDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGKGFYSRSPTF 409
DB 361 RLIDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGKGFYSRSPTF 409

RESULT 2

ID AAU29090 standard; protein; 409 AA.
XX
AC AAU29090;
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #67.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN W0200169848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186969P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006984.

PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 28-MAR-2000; 2000US-0193032P.
PR 28-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 28-AUG-2000; 2000US-02644848.
PR 28-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-602746/68.
N-PSDB; AAS45991.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the
presence of tumors, such as prostate and breast tumors, in mammals and to
screen for modulators of the compounds.

Claim 11; Fig 134; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
The PRO polypeptides and their associated nucleic acids can be used to
detect the presence of a tumour in a mammal by comparing the level of
expression of a PRO polypeptide in a test sample of cells from the animal
and a control sample of normal cells, whereby a higher level of
expression in the test sample indicates the presence of a tumour in the
mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
and rabbits but are preferably human. The polypeptides can be used to
stimulate tumour necrosis factor (TNF) alpha release from human blood,
when contacted with it. A specific polypeptide can be used to stimulate
the proliferation or differentiation of chondrocyte cells. The PRO
proteins can be used to determine the presence of tumours and also
susceptibility to tumour development, particularly adrenal, lung, colon,
breast, prostate, rectal, cervical, or liver tumours, in mammalian
subjects. The oligonucleotide probes specific for the PRO nucleic acids
can be used for genetic analysis of individuals with genetic disorders

Sequence 409 AA;

Query Match 100.0%; Score 409; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGSGFVLGALAFQHLNLTSDTEGFLGKGEAKNSITDSQMDVVEVYITD 60
DB 1 MEGESTSAVLGSGFVLGALAFQHLNLTSDTEGFLGKGEAKNSITDSQMDVVEVYITD 60

QY 61 IQKIYPCYQLFSFYNSGVEVNEQALKKILSNVKNVGVYKFRHRSDQIMTFRRERLLHKN 120
DB 61 IQKIYPCYQLFSFYNSGVEVNEQALKKILSNVKNVGVYKFRHRSDQIMTFRRERLLHKN 120
QY 121 LQEHFNSQDLVFLLLTPSIITESCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180
DB 121 LQEHFNSQDLVFLLLTPSIITESCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180
QY 181 TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQBELKSIKKVEDSQAV 240
DB 181 TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQBELKSIKKVEDSQAV 240
QY 241 DKLVDVNRLLKREIEKRRGAQIOAAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS 300
DB 241 DKLVDVNRLLKREIEKRRGAQIOAAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS 300
QY 301 LKNRVHSSKSCNHNHLDVVDNLTLMVHTDIPEASPASTPQIIKHKALDLDLDRWQFKRS 360
DB 301 LKNRVHSSKSCNHNHLDVVDNLTLMVHTDIPEASPASTPQIIKHKALDLDLDRWQFKRS 360
QY 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGFYSRSPTF 409
DB 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGFYSRSPTF 409
RESULT 3
ID AAB87536 standard; protein; 409 AA.
XX AAB87536;
AC AAB87536;
DT 15-MAY-2001 (first entry)
XX Human PRO1013.
DE Human; PRO protein; mapping.
KW Homo sapiens.
OS Homo sapiens.
XX WO200116318-A2.
XX 08-MAR-2001.
XX 24-AUG-2000; 2000WO-US023328.
XX 01-SEP-1999; 99WO-US020111.
XX 15-SEP-1999; 99WO-US021090.
XX 07-DEC-1999; 99US-0169493P.
XX 09-DEC-1999; 99US-0170262P.
XX 11-JAN-2000; 2000US-0175481P.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX 01-MAR-2000; 2000WO-US005601.
XX 03-MAR-2000; 2000US-0187202P.
XX 21-MAR-2000; 2000US-0191007P.
XX 30-MAR-2000; 2000WO-US008439.
XX 25-APR-2000; 2000US-0199397P.
XX 22-MAY-2000; 2000WO-US014042.
XX 05-JUN-2000; 2000US-0209832P.
XX (GETH) GENENTECH INC.
XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX N-PSDB; AA92068.
DR WPI: 2001-183260/18.
XX N-PSDB; AA92068.
DR Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.

XX Claim 12; fig 22; 278pp; English.
XX The present sequence is a human PRO polypeptide (secreted and
CC transmembrane) The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping
XX Sequence 409 AA;
SQ Query Match 100.0%; Score 409; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGESTSAVLGSLGALAFQHLNTDSDTEGFLGVEKGEAKNSITDSQMDVVEVYITID 60
DB 1 MEGESTSAVLGSLGALAFQHLNTDSDTEGFLGVEKGEAKNSITDSQMDVVEVYITID 60
QY 61 IQKIYPCYQLFSFYNSGVEVNEQALKKILSNVKNVGVYKFRHRSDQIMTFRRERLLHKN 120
DB 61 IQKIYPCYQLFSFYNSGVEVNEQALKKILSNVKNVGVYKFRHRSDQIMTFRRERLLHKN 120
QY 121 LQEHFNSQDLVFLLLTPSIITESCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180
DB 121 LQEHFNSQDLVFLLLTPSIITESCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180
QY 181 TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQBELKSIKKVEDSQAV 240
DB 181 TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQBELKSIKKVEDSQAV 240
QY 241 DKLVDVNRLLKREIEKRRGAQIOAAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS 300
DB 241 DKLVDVNRLLKREIEKRRGAQIOAAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS 300
QY 301 LKNRVHSSKSCNHNHLDVVDNLTLMVHTDIPEASPASTPQIIKHKALDLDLDRWQFKRS 360
DB 301 LKNRVHSSKSCNHNHLDVVDNLTLMVHTDIPEASPASTPQIIKHKALDLDLDRWQFKRS 360
QY 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGFYSRSPTF 409
DB 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGFYSRSPTF 409
RESULT 4
ID AAB65189 standard; protein; 409 AA.
XX AAB65189;
AC AAB65189;
DT 02-APR-2001 (first entry)
XX Human PRO1013 (UNQ496) protein sequence SEQ ID NO:158.
XX Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay.
XX Homo sapiens.
XX WO200073454-A1.
XX 07-DEC-2000.
XX 30-MAR-2000; 2000WO-US008439.
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 07-JUL-1999; 99US-0143048P.
XX 20-JUL-1999; 99US-0144758P.

Db	181	TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASYLOELKSIKCKVEDEQAV	240
QY	241	DKLVKDVNRLKKEIEKRRGAQIQAAAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS	300
Db	241	DKLVKDVNRLKKEIEKRRGAQIQAAAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS	300
QY	301	LKNRVKSSKSNYHHLVDVNDLTLVVEHTDIPEASPASTPOI IKKALDLDLRWQFKRS	360
Db	301	LKNRVKSSKSNYHHLVDVNDLTLVVEHTDIPEASPASTPOI IKKALDLDLRWQFKRS	360
QY	361	RLLDQDKSKANTGSSNQDKASKVSSPETDEIEKMKGFGEYSRSPTF	409
Db	361	RLLDQDKSKANTGSSNQDKASKVSSPETDEIEKMKGFGEYSRSPTF	409
RESULT 5			
ABG95861	standard; protein; 409 AA.		
ID	ABG95861		
XX	XX		
AC	ABG95861;		
XX	XX		
DT	10-DEC-2002	(first entry)	
XX	XX		
DE	Human secreted/transmembrane protein PRO1013.		
XX	XX		
KW	Human; secreted protein; transmembrane protein; antirheumatic;		
KW	antiarthritic; osteopathic; sports-related joint problem;		
KW	articular cartilage defect; osteoarthritis; rheumatoid arthritis.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
PN	US2002119130-A1.		
XX	XX		
PD	29-AUG-2002.		
XX	XX		
PF	06-DEC-2001; 2001US-00006867.		
XX	XX		
PR	29-OCT-1997; 97US-0063435P.		
PR	29-OCT-1997; 97US-0064215P.		
PR	22-APR-1998; 98US-0082797P.		
PR	29-APR-1998; 98US-0083495P.		
PR	15-MAY-1998; 98US-0085579P.		
PR	02-JUN-1998; 98US-0087759P.		
PR	04-JUN-1998; 98US-0088021P.		
PR	04-JUN-1998; 98US-0088029P.		
PR	04-JUN-1998; 98US-0088030P.		
PR	10-JUN-1998; 98US-0088734P.		
PR	10-JUN-1998; 98US-0088811P.		
PR	10-JUN-1998; 98US-0088824P.		
PR	10-JUN-1998; 98US-0088825P.		
PR	11-JUN-1998; 98US-0088863P.		
PR	12-JUN-1998; 98US-0089105P.		
PR	16-JUN-1998; 98US-0089514P.		
PR	17-JUN-1998; 98US-0089653P.		
PR	19-JUN-1998; 98US-0089952P.		
PR	22-JUN-1998; 98US-0090246P.		
PR	24-JUN-1998; 98US-0090444P.		
PR	25-JUN-1998; 98US-0090688P.		
PR	25-JUN-1998; 98US-0090896P.		
PR	26-JUN-1998; 98US-0090862P.		
PR	02-JUL-1998; 98US-0091628P.		
PR	10-AUG-1998; 98US-0096012P.		
PR	17-AUG-1998; 98US-0096757P.		
PR	18-AUG-1998; 98US-0096949P.		
PR	18-AUG-1998; 98US-0096959P.		
PR	26-AUG-1998; 98US-0097971P.		
PR	26-AUG-1998; 98US-0097979P.		
PR	01-SEP-1998; 98US-0098749P.		
PR	10-SEP-1998; 98US-0099741P.		
PR	10-SEP-1998; 98US-0099763P.		
PR	10-SEP-1998; 98US-0099792P.		

PR	26-JUL-1999;	99US-0145698P.	
PR	28-JUL-1999;	99US-0146222P.	
PR	17-AUG-1999;	99US-0149396P.	
PR	15-SEP-1999;	99WO-US021090.	
PR	15-SEP-1999;	99WO-US021547.	
PR	08-OCT-1999;	99US-0158663P.	
PR	30-NOV-1999;	99WO-US028313.	
PR	01-DEC-1999;	99WO-US028301.	
PR	16-DEC-1999;	99WO-US030095.	
PR	20-DEC-1999;	99WO-US030911.	
PR	05-JAN-2000;	2000WO-US000219.	
PR	06-JAN-2000;	2000WO-US000376.	
PR	11-FEB-2000;	2000WO-US003565.	
PR	18-FEB-2000;	2000WO-US004341.	
PR	22-FEB-2000;	2000WO-US004414.	
PR	24-FEB-2000;	2000WO-US004914.	
PR	24-FEB-2000;	2000WO-US005004.	
PR	02-MAR-2000;	2000WO-US005841.	
PR	15-MAR-2000;	2000WO-US006884.	
PR	20-MAR-2000;	2000WO-US007377.	
XX	PA	(GETH) GENENTECH INC.	
XX	XX		
PI	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;		
PI	Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski FJ;		
PI	Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;		
PI	Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;		
PI	Zhang Z;		
XX	XX		
DR	WPI; 2001-032160/04.		
DR	N-PSDB; AAF44145.		
XX	XX		
PT	PRO polynucleotides used to produce polypeptides used to target bioactive		
PT	molecules such as toxins, radiolabels or antibodies, to specific cells,		
PT	to cause targeted cell death.		
XX	XX		
PS	Claim 12; Fig 95; 935pp; English.		
XX	XX		
CC	The present invention describes human secreted and transmembrane PRO		
CC	proteins. The PRO proteins have cytostatic activity. The PRO proteins can		
CC	be used for targeted delivery of bioactive molecules, such as toxins,		
CC	radiolabels or antibodies, that cause cell death. PRO nucleotide		
CC	sequences, and their fragments, can be used as hybridisation probes, in		
CC	chromosomal and gene mapping, and in the generation of anti-sense RNA and		
CC	DNA. They may also be used to produce transgenic animals which are used		
CC	to develop and screen therapeutically useful reagents. The PRO nucleotide		
CC	and protein sequence can be used for tissue typing and in treating		
CC	cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to		
CC	AAF44470 represent PCR primers and hybridisation probes used in the		
CC	isolation of human PRO sequences. AAF44087 to AAF44269 and AAF65154 to		
CC	AAB65300 represent human PRO polynucleotide and protein sequences given		
CC	in the exemplification of the present invention		
XX	XX		
SQ	Sequence 409 AA;		
Query Match 100.0%; Score 409; DB 4; Length 409;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MEGESTSAVLGSLGALAFQHLNTSDTEGFLGKGEAKNSITDSQMDVVEVYITD	60
Db	1	MEGESTSAVLGSLGALAFQHLNTSDTEGFLGKGEAKNSITDSQMDVVEVYITD	60
QY	61	IQYIPCYQLFSPYNSGVEVNEQALKILSNVKNVGVGKFRHSDQIMTFRELLHKN	120
Db	61	IQYIPCYQLFSPYNSGVEVNEQALKILSNVKNVGVGKFRHSDQIMTFRELLHKN	120
QY	121	LQHFNSQDLVFLLLPSTITESCSFTHLEHSLYKPKGLFHRVPLVAVANLQMSQLGVK	180
Db	121	LQHFNSQDLVFLLLPSTITESCSFTHLEHSLYKPKGLFHRVPLVAVANLQMSQLGVK	180
QY	181	TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASYLOELKSIKCKVEDEQAV	240

CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence represents a novel secreted or transmembrane protein of the
CC invention
XX
SQ Sequence 409 AA;

Query Match 100.0%; Score 409; DB 5; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
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QY 61 IQYIFCYQLFSPYSSGVEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRERLLHKN 120
Db 61 IQYIFCYQLFSPYSSGVEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRERLLHKN 120
QY 121 LQEHFNSQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVNLGMSQGLYK 180
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QY 181 TVSGSCWSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASYLQELKSI CKKYDSEQAV 240
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QY 301 LKNRHYKSSCNVNHLDVVDNLTLVVEHTDIPASPASTPQIIKHKALDLDLRWQFKRS 360
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QY 361 RLDDTQDKRSKANTGSSNODKASKMSSPETDEIERKMGFGYSRSPTF 409
Db 361 RLDDTQDKRSKANTGSSNODKASKMSSPETDEIERKMGFGYSRSPTF 409

RESULT 6

ABUS8466
ID ABUS8466 standard; protein; 409 AA.

XX AC ABUS8466;

XX DT 15-APR-2003 (first entry)

XX DE Human PRO polypeptide #67.

XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.

PR 10-SEP-1998; 98US-0099812P.
PR 16-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 17-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
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PR 23-SEP-1998; 98US-0101475P.
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PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 98WO-US005028.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

XX (GETH) GENENTECH INC.

XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI,

XX MPI; 2002-731348/79.
DR N-PSDB; ABS74388.

XX New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.

XX Claim 20; Fig 22; 399pp; English.

XX The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ASG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, E/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises

XX OS Homo sapiens.
XX PN US2003027272-A1.
XX PD 06-FEB-2003.
XX PF 21-JUN-2002; 2002US-00176492.
XX PR 18-SEP-1997; 97US-0059263P.
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PR 17-OCT-1997; 97US-0082250P.
PR 21-OCT-1997; 97US-0083486P.
PR 24-OCT-1997; 97US-0063120P.
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PR 28-OCT-1997; 97US-0063540P.
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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.

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Query Match: 100.0%; Score 409; DB 6; Length 409;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEGESTSAVLGFLGALAFQHLNTSDTEGFLGVEKGEAKNSITDSQMDDEVVYITD 60

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QY	241	DKLVKDVNRLKREIEKRGAGIQAAAREKNIQKDPQENIFLQALRTFPNSEFLHSCVMS	300
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AC	ABU84329;		
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DT	02-AUG-2003 (first entry)		
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DE	Human secreted/transmembrane protein (PRO) #67.		
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KW	Human; secreted and transmembrane protein; PRO; TNF-alpha;		
KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;		
KW	tissue typing.		
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OS	Homo sapiens.		
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PN	US2003032112-A1.		
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PD	13-FEB-2003.		
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PF	21-JUN-2002; 2002US-00176756.		
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DB	121	LOEHFSNODLVFLLLTPSIITTESCSTHLEHSLYKPKGLFHRVPLVVANLGMSEQLGYK	180		
QY	181	TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMIASLOBELKSI CKKVEDSEQAV	240		
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QY	241	DKLVKDVNRLKHEIEKRRGAQIQAAAREKNIQDPOENIFLQALRTFFPNSEFLHSCVMS	300		
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Best Local Similarity 100.0%; Pred. No. 0;
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KW tissue typing.
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DT	14-APR-2003 (first entry)		
XX	Human PRO polypeptide #36.		
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KW	Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;		
KW	horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEP;		
KW	antibody-dependent enzyme mediated prodrug therapy.		
XX			
OS	Homo sapiens.		
XX			
PN	US2003027163-A1.		
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PD	06-FEB-2003.		
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PF	15-NOV-2001; 2001US-00997666.		
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PR 08-NOV-2000; 2000WO-US030952.
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PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Klijavin IJ, Napier MA, Par J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams EM, Wood WI;
PI Zhang Z;
XX WPI; 2003-247083/24.
DR N-PSDB; ABX80226.
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.
XX Claim 12; Fig 95; 648pp; English.
XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO825, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX Sequence 409 AA;
SQ Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGESTSAVLGSGVGLGALAFQHLNTSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60
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QY 61 IQKYPICYQLFSYNSGVEVNEQALKILSNVKNVGVGWYKFRHSDQIMTFRELLHN 120
Db 61 IQKYPICYQLFSYNSGVEVNEQALKILSNVKNVGVGWYKFRHSDQIMTFRELLHN 120
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XX AC ABU82594;
XX DT 26-JUN-2003 (first entry)
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DE Human; PRO; secreted protein; transmembrane protein;
XX cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; eight loss;
KW retinitis pigmentosa; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
KW Crohn's disease; sports injury; arthritis.
XX Homo sapiens.
XX US2003032023-A1.
XX 13-FEB-2003.
XX 14-NOV-2001; 2001US-00990711.
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
XX 05-NOV-1997; 97WO-US020069.
XX 12-NOV-1997; 97US-0065186P.
XX 13-NOV-1997; 97US-0065311P.
XX 24-NOV-1997; 97US-0066770P.
XX 25-FEB-1998; 98US-0075945P.
XX 20-MAR-1998; 98US-0078910P.
XX 28-APR-1998; 98US-0083322P.
XX 07-MAY-1998; 98US-0084600P.
XX 28-MAY-1998; 98US-0087106P.
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XX chromosome mapping; Gene mapping; cytostatic.
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OS Homo sapiens.
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PN US2003032113-A1.
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PD 13-FEB-2003.
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PF 20-JUN-2002; 2002US-00176911.
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XX KW chondrocyte differentiation; tumour necrosis factor-alpha release;
XX KW affinity purification.
XX OS Homo sapiens.
XX PN US2003036147-A1.
XX PD 20-FEB-2003.
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